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OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 03:27:38 ; Search time 10041 Seconds
(without alignments)
11561.706 Million cell updates/sec

Title: US-10-053-662A-1
Perfect score: 3989
Sequence: 1 tgggtccctctattacag.....ccagataaatgtcttatttg 3989

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapect 1.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:
1: gb_da:*
2: gb_htg:*
3: gb_in:*
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2986.2	74.9	5200	6 AX045561	AX045561 Sequence
2	2986.2	74.9	5200	6 162749	162749 Sequence 12
3	2986.2	74.9	5200	9 HSLAMB2T	AX045561 Sequence 12
4	2956.4	74.1	5156	6 AX365737	AX045561 Sequence 12
5	2956.4	74.1	5156	9 HSNICE	AX045561 Sequence 12
6	2944.2	72.8	3720	6 AX045565	AX045565 Sequence
7	2880.8	72.2	3620	6 AX045567	AX045567 Sequence
8	2879.2	72.2	5020	6 AX045563	AX045563 Sequence
9	2726	68.3	4316	6 162750	162750 Sequence 14
10	2726	68.3	4316	9 HSLAMB2TB	AX045569 Sequence
11	2652.2	66.5	5158	10 MMU33327	U43327 Mus musculus
12	2590	64.9	5159	6 AX045569	AX045569 Sequence
13	2537.4	63.6	5057	6 AX045571	AX045571 Sequence
14	860.2	21.6	1393	10 MUSNICC	L20477 Mus musculus
15	528.2	13.2	3020	5 AF373841	AF373841 Gallus ga
16	517.4	13.0	7642	10 MUSLAM2B	J03484 Mouse lamin
17	515.6	12.9	4948	6 AX045115	AX045115 Sequence
18	515.6	12.9	4948	6 AX045332	AX045332 Sequence
19	515.6	12.9	4948	6 AX463752	AX463752 Sequence
20	515.6	12.9	4972	6 AX045119	AX045119 Sequence
21	515.6	12.9	5306	6 AX045113	AX045113 Sequence
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28	514.6	12.9	7263	6 AX045336	AX045336 Sequence
29	514.6	12.9	7263	6 AX463756	AX463756 Sequence
30	514.6	12.9	7554	6 AX045121	AX045121 Sequence
31	514.6	12.9	7554	6 AX045334	AX045334 Sequence
32	514.6	12.9	7554	6 AX463754	AX463754 Sequence
33	514.6	12.9	7554	10 MUSLAM2A	J02930 Mouse lamin
34	464.2	11.6	6055	5 AF468048	AF468048 Danio rer
35	366.8	9.2	551	6 AX302928	AX302928 Sequence
36	350.2	8.8	5184	9 AF041835	AF041835 Homo sapi
37	285.8	7.2	5737	3 DBOLAMB2	M25063 Drosophila
38	284.4	7.1	4482	3 DKLAMB2	X07806 Drosophila
39	265.2	6.6	1778	6 AX335505	AX335505 Sequence
40	265.2	6.6	1778	9 HSLAMI24	U13201 Human lamin
41	265.2	6.6	164084	9 AL354953	AL354953 Human DNA
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43	263.6	6.6	220000	2 AC004795	AC004795 Homo sapi
44	239	6.0	5153	10 AF083372	AF083372 Mus muscu
45	234.8	5.9	4664	10 AF079520	AF079520 Mus muscu

ALIGNMENTS

RESULT 1
AX045561
LOCUS AX045561 5200 bp DNA linear PAT 24-NOV-2000
DEFINITION Sequence 25 from Patent WO0066731.
ACCESSION AX045561
VERSION AX045561.1 GI:11344011
KEYWORDS
SOURCE
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 5200)
AUTHORS
Boutaud, A.
TITLE
Recombinant laminin 5
JOURNAL
Patent: WO 0066731-A 25 09-NOV-2000;

QY	1712	CTTCGGGGAACGTGGCCCAAGTAGAGCCCTGTCAAGCCTGTCAAGTCAACAACAACGTGGA	1771
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Db	1689	CCCCAGTGCCTCTGTGGAAATGTGACCGCGCTGACAGGGAGGTGTGTAAGTGTATCCACA	1748
QY	1832	CACAGCTTGGGGTCCACATGTGACCAAGTGCACAAAGCAGGCTACTATGTGGGACCCGTTGGCTCC	1891
Db	1749	CACAGCCGGCATCTACTGTGCGACCAAGTGCACAAAGCAGGCTACTTGGGGAGCCATTGGCTCC	1808
QY	1892	CAATCCAGCAGACAGAAGTGTGTGAGCTTCACTGCAACCCAGTGGGCTCGAGGCTGTGGA	1951
Db	1809	CAACCCAGCAGACAAAGTGTGAGCTTCAACTGTAAACCCATGGGCTCAAGAGCCTGTGAG	1868
QY	1952	GTCGTCAAGAGTATGGCAGCTGTGTGTTTCAGCCAGCCTTGTGTGGGCTCAAGCTGTGACA	2011
Db	1869	ATGTCCGAAGTATGGCAGCTGTGTGTTTCAGCCAGATTTGTGTGCCCAACTGTGAGCA	1928
QY	2012	TGCGGCACTGACCAAGCTGTCCAGCTTGTCTAATAATCAATGAGAGTTCAATGATCAATT	2071
Db	1929	TGGAGCATTT--CAGCTGTCCAGCTTGTCTAATAATCAATGAAATTCAGATGATCAAGTT	1985
QY	2072	TATCAGCAGCTTCCAGATTCCTGGAGGCGCCGATTTGCAAGGCTCAAGG-----TGAGC	2125
Db	1986	TATCAGCAGCTTCCAGGAATGTGAGGCCCTGTGATTTCAAAAGGCTCAAGGCTGTATGAGT	2045
QY	2126	AGTACCCAGCAGCAGAGCTGGAAGGCAAGATGACAGCAGCTGAGCAGGCTCTTGCGGCAT	2185
Db	2046	AGTACCTGATACAGAGCTGGAAGGCAAGATGACAGCAGCTGAGCAGGCTCTTGCGGCAT	2105
QY	2186	TCCTGAGAAGGCCAGATTCACAAAGATGCTGTAGTTCCTTCAAATCCGGGTGGCCAA	2245
Db	2106	TCCTGAGAATGCCCCAGATTCACAAAGATGCTGTAGTTCCTTCAAATCCGGGTGGCCAA	2165
QY	2246	GGCAAGCACTCAAGAGAATAGCTACCCGGGAGCCGCTGTGATGACCTCAAGATGACTGTGA	2305
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QY	2306	AAGAGTTCCGGGCCCTTGGGGCACTAGTATCAGAAACCAAGTTCAAGTACTCGCAGGCTCAT	2365
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QY	2366	CACACAGATGGGCTGTGAGCCTGAGCGAGAAAGTAGAGCTTCCCTGTGCAAAACCAACATTC	2425
Db	2286	CACACAGATGAGCTGAGCCTGTGAGCGAGAAAGTAGAGCTTCCCTGTGGAACCACTAACATTC	2345
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QY	2600	CGGAAGGGGCGCCTTGAGAGCGAGCCGTGTGTCCAAAGGCTTGTGGGAAATTTGCGAAGAAC	2659
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QY	2660	TAAATCTCTGGCCCCAGAGTGTGTGAGGAGAGGCCACCAACCAATGAGAGCAGATAG	2719
Db	2586	CAAGTCCCTGGCCCCAGAGTGTGAGAACAGGAGGCCACATCAAGCGGAATTTGAAGCAGATAG	2645
QY	2720	GTCATTATCAGATATGTCTCCACCTTCTCAATTCCTGCTCTTCAGATTCAGGAGTCAATGA	2779
Db	2646	GTCATTATCAGACAGTCTCCGCTCTCTGTGATATAGTCTCTCCGCTCTCAGGAGTCAATGA	2705

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Db	2706	TCAGTCCCTTTCAGTGGGAAGGAAGAAAGGATCAACAAAACCGATTTCTCTCTCAAG	2765
QY	2837	CCGATGTACTAAGCATATATGATGAGTTCACACAGTGGCAAAACATCTGGGAAACTGGGA	2896
Db	2786	CCTGGTAAACACAGGCATATGATGATGATTCAACCTACACAAAAGAAATCTGGGAAACTGGAA	2825
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Db	2826	AGAAAGAACACAGCAGCTCTTACAGAAATGGAAGAAATGGGAGAGAAATCAGATCACT	2885
QY	2957	GCTTTCCTGGCCCAACTTGGTAAAGCAGAGCCCAAGAACACTAGTATGGGCATATGC	3016
Db	2886	GCTTTCCTGGCCCAACTTGGTAAAGCAGAGCCCAAGAACACTAGTATGGGCATATGC	2945
QY	3017	CACCTTTTATGAAGTTGAGAACATCTTAAAGAAATCTCAGAGAGTTTGACCTGCAGGTTTG	3076
Db	2946	CACCTTTTATGAAGTTGAGAACATCTTAAAGAAATCTCAGAGAGTTTGACCTGCAGGTTGA	3005
QY	3077	AGATTAAGAACACAGAGCTGAAGAGGCCATTAAGAGACTCTCTCTACATCAGCCAGAAAGT	3136
Db	3006	CACAGAAACACAGAGAGCTGAAGAGGCCATTAAGAGACTCTCTCTACATCAGCCAGAAAGT	3065
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Db	3066	TTTCAGATCCAGTGCACAGAGCAGAGACAGAGAACCCCTGGGCAGCTGCCTGCCTGA	3125
QY	3197	CGCCACAGGCGCAAGAAATGCAGCCAGGAGGCCCTGGAGATCTCTGGCAAGATTAACA	3256
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QY	3317	GAAGGACTGGCCACTCTGAAAGAGTGAGATGAGAGAAATGGAGAGAGCTGTCAAGGAA	3376
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QY	3617	AGAGCTGGAAGAGAGGACATCGGACAGAAAGGCCACTCCGTTTCTGTGAGATTCAGAT	3677
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LOCUS	162749	162749	5200 bp	DNA	Linear	PAT 07-OCT-1997
DEFINITION	Sequence 12 from patent US 5660982.					
ACCESSION	162749					
VERSION	162749.1	GI:2480457				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 5200)					
AUTHORS	Trygveason, K., Kallunki, P. and Pyke, C.					
JOURNAL	Laminin chains: diagnostic uses					
FEATURES	Patent: US 5660982-A 12-26-AUG-1997;					
	Location/Qualifiers					
	source	1..5200				
		/organism="unknown"				
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ORIGIN						
Query Match	74.9%;	Score 2986.2;	DB 6;	Length 5200;		
Best Local Similarity	88.5%;	Pred. No. 0/;				
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72	AGCGACCCCTCAGCGCGCGCGAGACAGAGACTGAGCGCGCGCGCGCGCGCGCGCGCTG	131				
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132	GCTGCGCGCTGCGCTG	191				
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192	GGAAGTCTGTATTGTCACAAATGGGAGATCCAGGCAAGTATCTTTGATCGGAACTTCACAG	251				
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432	ACCAAGTCTGACAGGAGACAGGTGACCGATGCTGCGCGCTTCCACACACTCACATGCA	491				
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Db 1889 ATGTGAAATGATGACCTGTGTGTGCAAGCCAGATTTGTGGCCCACTGAGACA 1928
QY 2012 TCGCGACTGACAGCTTCAGCTTGTCTATATCAATGAAGTGAAGTTCAGATGATGAT 2071
Db 1929 TGGAGCATTT---CAGCTGTCCAGCTTGTCTATATCAATGAAGTTCAGATGATGATGAT 1985
QY 2072 TATGAGCAGCTCCAGATCTGTGAGAGCCCTGATTTGCAAGGCTCAGGG-----TGAAGC 2125
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QY 3797 GGTCTTGGAGATCAG 3837
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RESULT 3
HSLAMB2T
LOCUS H.sapiens mRNA for laminin. 5200 bp mRNA linear PRT 27-MAR-1996
DEFINITION
ACCESSION Z15008.547028
VERSION Z15008.1 GI:34229
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 5200).
Kallunki,P., Sahlro,K., Eddy,R., Byers,M., Kallunki,T., Sariola,H.,
Beck,K., Hironen,H., Shows,T.B. and Tiryagvason,K.
A truncated laminin chain homologous to the B2 chain: structure,
TITLE

spatial expression, and chromosomal assignment
JOURNAL J. Cell Biol. 119 (3), 679-693 (1992)
MEDLINE 93016279
PUBMED 1383240
REFERENCE 2 (bases 1 to 5200)
AUTHORS Tryggvason, K..
TITLE Direct Submission
JOURNAL Submitted (27-AUG-1992) Tryggvason K., Biocenter and University of
Oulu, Biochemistry, Linnaumaa, Oulu, Finland, SF-90570
location/Qualifiers
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Oy 3184 GTGCTGTCCGAGCCCGAGAGGCGCAAGATGACAGCAGAGGAGGCGCTGAGATCTCG 3243
Db 3061 GCGCTGTGCTGATCAGAGAGGCGCAAGATGAGGCGGAGGCGCGCTGGAATCTCCA 3120
Oy 3244 GCAAGATGAACAGAGATGAGAGGCTGCAACTGTGGAAGCCAAATGTGACAGAGTGGAG 3303
Db 3121 GGAAGATGAACAGAGATGAGAGGCTGCAACTGTGGAAGCCAAATGTGACAGAGTGGAG 3180
Oy 3304 CTTTGGCATGAGAGAGGAGTGGCCACTGCTTGAAGATGAGATGAGAGAGAGAGAG 3363
Db 3181 CTTTGGCATGAGAGAGGAGTGGCCACTGCTTGAAGATGAGATGAGAGAGAGAGAGAG 3240
Oy 3364 AGCTGTCAAGAGAGAGAGAGTGTGACAGATGATGAGAGAGAGAGAGAGAGAGAG 3423
Db 3241 AGCTGTCAAGAGAGAGAGAGTGTGACAGATGATGAGAGAGAGAGAGAGAGAGAG 3300
Oy 3424 CAGAGCCCAAGAGATGTAAGAAACAGAGCAAGATGTGAGAGTGTGAGATCCAGAGACAC 3483
Db 3301 CAGAGCCCAAGAGATGTAAGAAACAGAGCAAGATGTGAGAGTGTGAGATCCAGAGACAC 3360

[illegible]

OY		2282	GGATGACCTTAAGATGACTGTGGAAAGATTGGGGCCCTCGGCACATCAATGCAAAACA	2341
Dd		2122	GGATGACCTTAAGATGACTGTGGAAAGATTGGGGCCTGTGGAAATCATGATCCGAACCG	2181
OY		2342	AGTTCAAGATACTCGCGAGGCTCATCTCACTAAGTGGGCCGAGCCCTGGAGGAAAGTGAGGC	2401
Dd		2182	AGTTCCGGGATACCTCACAGGCTCATCTCACTAAGTGGAGCTGAGCCCTGGAGGAAAGTGAGGC	2241
OY		2402	TTCCCTCGCAAAACACCACAACTTCCTCTCTCAGAGCACTACGTTGGGGCCCAATGGCTTTAA	2461
Dd		2242	TTCCCTTGGGAAACACTAACATTCTCTCGCTCAGACACACTACGTTGGGGCCCAATGGCTTTAA	2301
OY		2462	AAGTTGGCTCAGAGGCCACGAGATTGGCGAGACACCATTGTCACTGACGCCATACAT	2521
Dd		2302	AAGTTGGCTCAGAGGCCACCAAGATTACAGAAAAGCCACGTTGATGATCAGCCAGTAACAT	2361
OY		2522	GGACCACTCGGCAAAAGGAAACCCAGGAGTATTCCAAAGGCTGATGTCACTGGTGGCGGA	2581
Dd		2362	GGACCACTCGGCAAAAGGAAACCTGAGAGCTATTCCAAACAGCCCTCTCACTAGTGGCGCA	2421
OY		2582	GGCCTCTCAGGAAGAG-----GCCGAAGCGGACACGCTGAGCGAGGCCGTTGGTCAAG	2635
Dd		2422	GGCCCTCATGAAGAGAGTGGGAAGCGGAAGCGGTAGCCGAGCGGTGCTGGTGGTCAAGG	2481
OY		2636	GCTTGTGGGAAATTGCGAAAACTTAATCTCTGGCCCAGAGGTTGTGAGGGAGGCCAC	2695
Dd		2482	GCTTGTGGAAAAATTGGAGAAAAACAAGTCCCTGGCCCCAGGTTGGTACAAAGGAGGCCAC	2541
OY		2696	GCAACGACATGGGAACACATAGTGCTTATCAGCACTAGTCCACCTTCCAAATTCCTCGT	2755
Dd		2542	TCAAGCGGAATTTGAAACAGATAGGCTTATCAGCACTATCTCCGCTCTTGGATTACGT	2601
OY		2756	GTCTCAATTCAGGGAGTCAATGATCACTCTTGACAGT--AGAAGCGAAGGCCCTCAG	2812
Dd		2602	GTCTCCGCTTCAGGAGATCAGTATCATGCTCTTCAAGTGGAAAGAAAGCAAGAGGATCAA	2661
OY		2813	ACAAAAGCTGATTTCTCTCAAAACCGTGTACTAACTATGATGATGATTCAGCACAGT	2872
Dd		2662	ACAAAAGCGGATTCATCTCCAAGCCTGGTAAACAGGCAATATGATGATGATTCACACCTTAC	2721
OY		2873	GCAAGCAATCTGGGAACTGGGAAAGGGAAGAAACCCGGGAGCTTACAGAAATGGGAAATA	2932
Dd		2722	ACAAAAGCAATCTGGGAAACTGGGAAAGGGAAGAAAGCACAGCTTACAGAAATGGGAAATA	2781
OY		2933	TGGGAGACAGATCAATCAGTACGCTGCTTCCGCTGCAACCTTGCATAAAGCAGAGCCCA	2992
Dd		2782	TGGGAGAGAGAAATCAGATCAGTGCCTTCCGCTGCCAATCTTGTCTAAAAGCAGAGCACA	2841
OY		2993	AGAAGCACTAAGTAGTAGGGCAATGCCACTTTTTATGAAAGTTGAAACATCTTAAAGATCT	3052
Dd		2842	AGAAGCACTAAGTAGTAGGGCAATGCCACTTTTTATGAAAGTTGAAAGATCTTAAAAAAGCT	2901
OY		3053	CAGAGAGTTTGACCTGCAAGTGTGGAAGATTAAGAGACGAAGCTGGAAGGCCATTAAGNG	3112
Dd		2902	CAGAGAGTTTGACCTGCAAGTGTGGAACAACAAAAAGCAGAAAGCTGGAAGGCCATTAAGAG	2961
OY		3113	ACTCTCCATCATCAGCCAGAGGCTGAGCTGCTGCAAGAGACAGCAAGCAGAGGAGG	3172
Dd		2962	ACTCTCTCATCTCAGCCAGAGAGTTTTCAGATGCTCCATGTGCAAGACCCAGCAAGCAGAGG	3021
OY		3173	AGCCCTGGGCAAGTGTCTGCTCGACAGCCCGCAGAGGCGCAAGAAATGCAAGCCAGGAGGCCCT	3232
Dd		3022	AGCCCTGGGGAAGGCTGTCTGCTGATGACAGAGGCGCAAGAAATGGGGCCCGGGAGGCCCT	3081
OY		3233	GGAGATCTCTGGCAAGATAGAACAGAGATAGSAGTCTGAACTTGGAAAGCCATATGTGAC	3292
Dd		3082	GGAAATCTCCAGTGAAGATTTGMAAGAGAGATTGGAGCTTGAACTTGGAAAGCCAAATGTAC	3141
OY		3293	AGCAGATGGAGCCTTGGCCATGGAGAAAGGACATCGGCATCTGAAAGTGAATGATGAGAA	3352
Dd		3142	AGCAGATGGAGCCTTGGCCATGGAGAAAGGAGATGCGCTCTCTGMAAGATGAGATAGGGA	3201
OY		3353	AGTGAAGAGAGCTGTGCAAGGAGAGGACGAGATTTGACATGATGATGAGACGAGTCA	3412

Db	841	CCACTTGGCAAGACACTBCTTGTGGGCTCACCAAGACTTACACATTACAGTTAAATGAC	900
OY	1161	CATCCAAAGCACTAAATTGGAGCCCCAGCTAAGTACTTGTAGATTCGAGAGTACTCGG	1220
Db	901	CATCCAAAGCACTAAATTGGAGCCCCAGCTGAGTTACCTTGTAGTATCGAAGGTTACTGGG	960
OY	1221	AACCTCACAGCCCTGCGGATCCGAGCTACCTACGAGAGATATCAGTACTGGGTACATTGAC	1280
Db	961	AACTCTCACAGCCCTCCCGCATCCGAGCTACATATGTGAGAAATACAGTACTGGGTACATTGAC	1020
OY	1281	AACGTGACCTTGATTTACGCCCCGGCCGTTCTGAGAGCCCAAGGCCCTGGGTTGACAA	1340
Db	1021	AATGTGACCTTGATTTACGCCCCGGCCGTTCTGTGAGAGCCCAAGACCTGGGTTGAAACAG	1080
OY	1341	TGTGTATATGCCCTGTTTGGCTACAAAGGGGCAAGTCTGCACAGATTTGTGCTCCGGCTACAAA	1400
Db	1081	TGTATATATGCTCTGTTGGGTACAAAGGGGCAATTTCTGCCAGATTTGTGCTTCGGCTACAG	1140
OY	1401	AGAGATTCAGCCAGACTGGGACCTTTTGGCACCTGTATTCAGTATTCAGTCCGAAGGGGGA	1460
Db	1141	AGAGATTCAGCGAAGACTGGGGCCCTTTTGGCACCTGTATTCCTTGAATCTCAAGGGGGA	1200
OY	1461	GGGGCCCTGGCATCCAGACACAGAGAGACTGTACTCAGGGGATGAGAAACCTGCATCCCT	1520
Db	1201	GGGGCCCTGTGATCCAGACACAGAGAGATTGTTATTACAGGGGATGAGAAATCCAGACAT--T	1257
OY	1521	GAGTGTGCTGACTGCCCATTTGTTTCTACAAAGCATCCAAAGACCCCGGAGCTGCAG	1580
Db	1258	GAGTGTGCTGACTGCCCATTTGTTTCTACAAAGCATCCGACAGACCCCGGAGCTGCAG	1317
OY	1581	CCGTGCCCTGTGCATGAGGGTTGACGTCTCCGTATGCTCTGAGACAGAGAGGTGGTG	1640
Db	1318	CCAGTGCCTGTGCATTAAGGGTTGACGTCTCAGTGAATGCCGAGAGCGGAGAGAGGTGGTG	1377
OY	1641	TGCATTAATCTGCCCCAGGGTGTACTGTGTGCCGCTGTGAGCTCTGTGTGATGGCTAT	1700
Db	1378	TGCATTAATCTGCCCTCCCGGGGTTGACCGGTGCCGCTGTGAGCTCTGTGTGATGGCTATC	1437
OY	1701	TTTGGGGAGCCCTTCGGGGAAGTGGGCCAGTGAAGGCTTTCAGAGCCCTGTCACTGCAC	1766
Db	1438	TTTGGGGAGCCCTTTGGTGAACATGGGCCCAATGAGGCTTTCAGAGCCCTGTCAATGCAAC	1497
OY	1761	AACAACGTGAGACCTAGTCCCTCCGGGAACTGTGACCCCTGCAGACAGGAGGTGCTGAAAG	1820
Db	1498	AACAATGTGAGACCCAGTCCCTTCGGGAATTTGTACCCGGCTGCAGACGAGAGGTGTTGAAG	1557
OY	1821	TGCTCCACAAACACAGCTGGGGTCCACTGTGACAGTGAAGTCAAGCAGGCTACTATGGGAC	1880
Db	1558	TGTATCCAAACACAGCCGCGCATCTACGTGCACAGTCAAGCAGGCTACTTCTGGGGAC	1617
OY	1881	CCGTTGGGTCCCAATCCAGGAGACAGTGTGAGGCTTTCACATCGAACCCAGTGGGCTCG	1940
Db	1618	CCATTGGTCCCAACCCAGCAGACAGTGTGAGGCTTTCACATCGTAACCCAGTGGGCTCA	1677
OY	1941	GAGCCTGTGAGAGTGTGCAAGTATGATGGGACGTGTGTTTCAAGCCAGGCTTTGTGGGCTTC	2000
Db	1678	GAGCCTGTGAGAGTGTGCAAGTATGATGGGACGTGTGTTTCAAGCCAGGATTTGTGGGCCCC	1737
OY	2001	AGCTGTGAGCATGGGGCACTGACAGCTGTCCAGCTTGTATTAATCAAGTAAGGTTACAG	2066
Db	1738	AACGTGTGAGCATGGGACATTT--CAGCTGTCCAGCTTGTATTAATCAAGTAAGTACAG	1794
OY	2061	ATGATATCGTTTATTCACAGACTCTCCAGATCTCGAGAGGCCGTGATTTGCAAGGCTCAGGG-	2119
Db	1795	ATGATATCGTTTATTCACAGACTCTTCAGGAATGGAGGCCGTGATTTCAAAGGCTCAGGGT	1854
OY	2120	-----TGAGCAGTATCCCAAGCAGAGAGTGGAAAGCAGATGCAGACAGGCTGAGCAGGCC	2174
Db	1855	GGTGATGAGATGATACCTGATACAGAGCTGGAAAGCAGAGATGCACAGGCTGACAGGCC	1914
OY	2175	CTTGGGGACATTTGAGAGAAAGCCAGATTTACAAAGATGCTGTTAGATTCCTTCAATCTC	2234

Db	1915	CTTGAAGCAATTCGTGAGAGATGCCCAAGATTTCCAGAAGTGTCTACAGATATCCCTTGCTC	1974
QY	2235	CGGGTGGCCAAAGGAGACTCAAGAGAAATGCTACCGGGAGCCGCTTGATGATCTCAAG	2294
Db	1975	CAGTTGGCCAAAGTGTGAGGAGCCAAAGAGAAACAGCTACCAAGACCGCTTGATGATCTCAAG	2034
QY	2295	ATGACTGTGGAAAGATTCCGGGCCCTGGGACGTCAATATCCGAACCAAGTTCCAGATTAAT	2354
Db	2035	ATGACTGTGGAAAGATTCCGGGCCCTGGGAGGTCAATATCCGAACCAAGTTCCAGATTAAT	2094
QY	2355	CGCAGGCTCAATCAGTCAAGATGCGGCTGGAGCCCTGGAGGAAATGTAGGGCTCCCTGCAAAAC	2414
Db	2095	CACAGCTCAATCAGTCAAGATGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG	2154
QY	2415	ACCAACATTCCTCCTTCAGAGCACTACGTGGGGCCAAATGGCTTTAAAGTCTGGCTCAG	2474
Db	2155	ACTAACAATTCCTGGCTCAGACCACTACGTGGGGCCAAATGGCTTTAAAGTCTGGCTCAG	2214
QY	2475	GAGGCCAGCAATTTGGCAGACAGCCATGTTAGTCAAGCAATGAGCAATGAGCAACTGGCA	2534
Db	2215	GAGGCCAGCAATTTAGCAGAAAGCCACGTTGAGTCAAGCAATGAGCAACTGAGCA	2274
QY	2535	AAGGAACCCAGGAGTATTTCCAAAGAGCTGATATGTCATGTCGAGGCGGAGGCTCTGCAAGAA	2594
Db	2275	AGGGAACCTGAGAGCTATTTCCAAACAGACCCCTCTCAGTGTGCGCAAGGCGCTGATGAA	2334
QY	2595	GGAG-----CGGGAAGCGGAGCGCTGGACGAGACCGGTGGTCAAAAGGCTTGTGGGAAA	2648
Db	2335	GGAGTCGGAACCGGAGGCGGTAGCCCGGACGCTGTGTGTGTCGAAGGCTTGTGGAAAA	2394
QY	2649	TTGCAGAAACTAAATCTTGTGGCCGAGAGTTGTGAGGAGGAGCCACGCAAAACCGACATG	2708
Db	2395	TTGGAGAAACCAAGTCCCTGTGGCCAGAGTTGACAAAGGAGGCGACATCAAGCGGAATTT	2454
QY	2709	GAAGCAATAGTCTTATCAGACATATGTTCCACCTTTCATTCCTGCTCTCAGATTTAG	2768
Db	2455	GAAGCAATAGTCTTATCAGACATATGTTCCACCTTTCATTCCTGCTCTCAGATTTAG	2514
QY	2769	GGAGCAATAGTCTTGTGCTGAGGT---AGAAAGGAGAGAGCTCAGACAAAGAGCTGAT	2825
Db	2515	GGAGTCAATGATCACTCTTTCAGTGTGGAAGAGCAAGAGAGATCAACCAAAAGCGAT	2574
QY	2826	TCTCTCTCAAAACCGTGTGACTAAGCATATGATGATGATTCGAAGCACTGCAAAAGCATGTG	2885
Db	2575	TCAGTCTCAAAACCGTGTGACTAAGCATATGATGATGATTCGAAGCACTGCAAAAGCATGTG	2634
QY	2886	GGAACCTGGAGAGAAAGAACCCGGCAGCTTTACAGATTTGGAAGATGGGAGACAGCA	2945
Db	2635	GGAACCTGGAGAGAAAGAACCCGGCAGCTTTACAGATTTGGAAGATGGGAGAGAGAAA	2694
QY	2946	TCAGATCAGTGTCTTCCCGTGGCCAACTGCTTAAGCAAGAGCCCAAGAGAGCACTAGT	3005
Db	2685	TCAGATCAGTGTCTTCCCGTGGCCAACTGCTTAAGCAAGAGCCCAAGAGAGCACTAGT	2755
QY	3006	ATGGCAATGCGCACTTTTATGAATTGAGAATCTTAAAGATCTCAGAGAGTTTAC	3065
Db	2755	ATGGCAATGCGCACTTTTATGAATTGAGAATCTTAAAGATCTCAGAGAGTTTAC	2814
QY	3066	CTGCAGGTTGGAGATTAAGAGACAGAACTGAAGAGCCATGAGAGACTCTCTACATCT	3122
Db	2815	CTGCAGGTTGGAGATTAAGAGACAGAACTGAAGAGCCATGAGAGACTCTCTACATCT	2874
QY	3126	AGCCAGAAAGTTGCGAGTGGCCAGTACAAAGAGCAAGAGCAAGAGCAAGAGCAAGAGCAAG	3188
Db	2875	AGCCAGAAAGTTTTCAGATGCCAGTACAAAGCCAGCAAGCAAGAGAGAGCCCTTGGGAGAC	2933
QY	3186	GCTGCTGCCGAGCCCAAGAGGCAAGAAATCAGACAGAGGAGGCGCTTGAGATCTCTGCG	3245
Db	2935	GCTGCTGCCGAGTTCAGATGCCAGTACAAAGCCAGCAAGCAAGAGAGAGCCCTTGGGAGAC	2994
QY	3246	AAGATAGAACAGAGATAGAGGTTCTGACTTTGGAAGCAATGTGACAGCAGATGAGACC	3305
Db	2995	GAGATTTGAACAGAGATTTGGAGATTTGGAATTTGGAAGCAATGTGACAGCAGATGAGACC	3054

OY	1101	CCACTTGAACAAGACACTGCCCTTGTGGGATCAACCAAGACTTACACATTCACATTAAATGA	1160
Db	841	CCACTTGGCAAGACACTGCCCTTGTGGGCTTCCACCAAGACTTACACATTCAGGTTAAATGAG	900
OY	1161	CATCAAGACATTAATTGGAGCCCCCAGCTAAGTACATTGAGTATGGAGGTTACTCTGCG	1220
Db	901	CATCAAGACATTAATTGGAGCCCCCAGCTAGTTACTTTGATGATCGAAGGTTTACTCTGCG	960
OY	1221	AACCTCAAGCCCTGCGGATCCGAGCTACCTACGAGGAATACACTACTGGGTACTATTGAC	1280
Db	961	AATCTCAAGCCCTCCGCGATCCGAGTACATATGATGAGAAATACACTACTGGGTACTATTGAC	1020
OY	1281	AACCTGACCTTGATTTACAGCCCCCGCTTCTGTAGACCCCGAGCCCTGGGTGAACA	1340
Db	1021	AATGTGACCCCTGATTTACAGCCCCCGCTCTGTAGACCCCGAGCAACCTGGGTGAACA	1080
OY	1341	TGTTATATGCCCTGTGTGGCTACAAAGGGGACAGTTCGCGAGATTGTGCTCCGGCTACAAA	1400
Db	1081	TGTTATATGCTCTGTGTGGGTACAAAGGGCAATTCGCCAGATTGTGCTTCGGGCTACAA	1140
OY	1401	AGACATTCAGCCAGACACTGGGACCTTTTGGCACCTGTATTCCATGTAACTGCGCAAGGGGA	1460
Db	1141	AGACATTCAGGAGACACTGGGGCTTTTGGCACCTGTATTCCTTGTAACTGTCAAGGGGGGA	1200
OY	1461	GGGGCCGTGGCCAGACACAGGAGAGCTACTACAGGGAGTGAAGAACCCGTGACATCCT	1520
Db	1201	GGGGCCGTGTGTATCCAGACACAGGAGATTTGTTATTCAGGGAGTGAAGAAATCCGTGAAT--T	1257
OY	1521	GAGTGTCTGACTGCCCATTTGGTTTCTACAAAGATCCACAAGACCCCGCAGCTGCAG	1580
Db	1258	GAGTGTCTGCTACTGCCCAATTTGGTTTCTACAAAGATCCGACAGACCCCGCAGCTGCAG	1317
OY	1581	CCGTGGCCCTGTGCCAATGGSTTATAGCTGCTCCCTGATTCCTTGAGACAGAGAGTGGTG	1640
Db	1318	CCATGTCCCTGTCTAACAGGGTTCAGCTGCTCACTGATTCGAGAGAGGAGAGTGGTG	1377
OY	1641	TGCATATACTGCCCCCAGGAGTGTCACTAGTGCCCGCTGTGACTGCTGTGAGTAT	1700
Db	1378	TGCATATACTGCCCTCCCGGGGTACACGGGTGCCGGCTGTGACTGCTGTGAGTAT	1437
OY	1701	TTTGGGGACCCCTTTCGGGGAAAGTGCGCCAGTGAAGCCCTTGTCAAGCTGTCAATGCAAC	1760
Db	1438	TTTGGGGACCCCTTGTGGGAAACATGAGGCCCACTGAGGGCTTGTCAAGCTGTCAATGCAAC	1497
OY	1761	AACAAGCGAGACCTAGTGCCTCCGGGAAACGTACACGCCCTGAGAGGAGAGTGTCTGAG	1820
Db	1498	AGCAATGTGGACCCCAATGCTCTGTGGGAATTTGTACCGGCTGACAGAGGAGAGTGTCTGAG	1557
OY	1821	TGCAATCCACAACACAGCTGGGGGTCCACTGTGACAGTGCAAGGCAAGGCTACTATGGGAC	1880
Db	1558	TGTAATCCACAACAACAGCCGCGCATCTACTGCGACAGTGCAAAAGGAGGCTACTTGGGGAC	1617
OY	1881	CCGTTGGCTGCCAATTCACAGACAGAGTGTGACTTGTCAATCGAACCCAGTGGGCTCG	1940
Db	1618	CCATTGGCTCCCAACCCAGACAGACAGTGTGACTTGTCAACTGTAAACCCATGGGCTCA	1677
OY	1941	GAGCCTGTGAGTGTGCAAGTGTAGTGGCAGCTGTGTGTTTGCACAGCCAGGCTTGTGGGCTC	2000
Db	1678	GAGCCTGTGAGTGTGCAAGTGTAGTGGCAGCTGTGTGTTTGCACAGCCAGGCTTGTGGGCTC	1737
OY	2001	AGCTGTAGACATGGGGCACTAGCAACAGCTGTCCAGCTTGTCTTAATCAAGTCAAGGTTTAC	2060
Db	1738	AACGTGTGACATGGAGCACTT--CAGCTGTCCAGCTTGTCTTAATCAAGTCAAAATTCAG	1794
OY	2061	ATGATATCAGTTTATGACACAGCTCCAGATCTCTGGAGGGCCGATTTTGCAGAGCTCAGGG-	2119
Db	1795	ATGATATCAGTTTATGACACAGCTTCCAGAGATGAGAGGCCCTCGATTTTCAABAGCTCAGGGT	1854
OY	2120	-----TGAGCAGTATCCCAACGCAAGAGCTGGAAGGCAAGATGACAGAGCTGTAGCAGGCC	2174
Db	1855	GGTATGATGATAGTATGATATACAGAGCTGTGCAAGGCAAGATGACAGAGGCTGTAGCAGGCC	1914

QY	2175	CTTGGGACATTTCTGAGAGAAAGCCAGATTTTACAAAGTGTGTTAAATCTTCAATCTC	2234
Db	1915	CTTCAGGACATTTCTGAGAGATGCCAATTTCAAAAGTGCTTACAGATCCCTTGCTC	1974
QY	2235	CGGGGGCCAAAGGCGAAGGACTCAAGAGATATGTACCGGGGACCGCTGGATGACCTCAAG	2294
Db	1975	CAGTTGGCCAAAGGTGAGAGGCCAAGACAAGCTACCAAGAGCCCGCTGGATGACCTCAAG	2034
QY	2295	ATGACTGTGCAAAAGTTCCGGCCCTTGGGGCAGTCAATCAAGCAAACTTCAGATACT	2354
Db	2035	ATGACTGTGCAAAAGATTCGGGCTCTGGGAAGTCAATGCCAAGACGATTCGGGATACT	2094
QY	2355	CGCAGGCTCATCTACTCAGAGATCGCCTGAGCCTGGAGAAAGTAGGCTTCCCTGCAAAAC	2414
Db	2095	CACAGGCTCATCTACTCAGATCAGATCAGCTCGCACAAGAAAGTGAAGCTTCCTGGGAAC	2154
QY	2415	ACCAACATTCCTCCTTCAAGACCTACTAGTGGGGCCAAATGGCTTTAAAGCTGCGCTCAG	2474
Db	2155	ACTAACATTCCTGCTCTCAGACCACTACGTGGGGCCAAATGGCTTTAAAGCTGCGCTCAG	2214
QY	2475	GAGGCGACAGATTTGGCAGCAGCCATGTTTCAGTCACGCCAGTAACATGAGACAAGCTGGCA	2534
Db	2215	GAGGCGACAAATTTAGCAGAAAGCCAGCTTGAATGACGCCATACATGAGACAAGCTGACA	2274
QY	2535	AAGGAAACCCAGAGATTTCCAAAAGCTGATGTCTACTGTGTGCGCGAGGCTCTGCAAGAA	2594
Db	2275	AGGGAAGATGAGACTATTTCCAAAAGCCCTCTCACATGGTGGCCAGAGCCCTCATGAA	2334
QY	2595	GGAG-----GCGGAAGCGGCAAGCCTGGACGGAGCCGTGGTGCAAAGCCTTTGGGAAAA	2648
Db	2335	GGAGTCGGAAACGGGAAGCGGTGAAGCCGAGACGCTCTGTGGTGCAAAGGCGTTGTGGAAAA	2394
QY	2649	TTGCGAAGAACTAAATCTCTGGCCAGAGATGTCGAGAGGGAGGCGACAGCAAAACGCAGATG	2708
Db	2395	TTGGAAGAAACCAAGTCCCTGGCCACAGAGTGTGCAAAGGAGGCGACTCAAGCGGAATT	2454
QY	2709	GAAGCAGATAGGTCTTATCAGCATATGTCCTCACCTTCTCAATTCGCTGTCTCAGATTGAC	2768
Db	2455	GAAAGATAGGTCTTATCAGCACACAGTGTCCGCTCGTGATTCAGTGTCTCCGCTTCAG	2514
QY	2769	GGAGTCAATGATCAAGTCTTTCAGCT---AGAACGAAAGGCTCAGACAAAAGCTGAT	2825
Db	2515	GGAGTCAATGATCAAGTCTTTCAGGTGGAAGAACCAAGAGATCAAAACAAAAGCGGAT	2574
QY	2826	TCTCTCTAAACCGGTGACTTAAGCATATGTGATGATGTTCAAGCAAGTCAAAAGCAACTG	2885
Db	2575	TCACTCTAAACCTGTGTAACAGGATATGTGATGATTTCAAGCCTTACACAAAAGAAATCTG	2634
QY	2886	GGAAACTGGGAAGAAAGAACCCGGCAGCTCTTACAGATGGAAGAAATGGGAGACAGACA	2945
Db	2635	GGAAACTGGAAAGAAAGAACGACAGAGCTCTTACAGAAATGGAAGAAAGGGAGAGAGAA	2694
QY	2946	TCAGATCAGTGTCTTCCCTGTCACACCTTCTTAAAGCAGAGCCCAAGAGACTAATG	3005
Db	2695	TCAGATCAGTGTCTTCCCTGTCACACCTTCTTAAAGCAGAGCCCAAGAGACTAATG	2754
QY	3006	ATGGGCAATGGCACTTTTATGAAGTTGAGAAACCTTAAAGAAATCAGAGAGTTTGAC	3065
Db	2755	ATGGGCAATGGCACTTTTATGAAGTTGAGAGCAATCTTAAAGAACTCAGAGATTTGAC	2814
QY	3066	CTGCAGTTGAGATATAAAGAGACAGAGCTCAAGAGGCGATGAAGAGACTCTCTACATC	3125
Db	2815	CTGCAGTTGAGAACACAGAAAGACAGAACTGAAAGAGCATGAAGAGACTCTCTACATC	2874
QY	3126	AGCCAGAAAGTTGCAAGTGCATGACAAAGACGAAGCAAGCAGAAAGCAAGCCTTGCGACT	3185
Db	2875	AGCCAGAAAGTTTTCAGATGCCAGTGCACAAAGCCAGCAAGCAAGAAAGAGCCTTGCGAGC	2934
QY	3186	GCTGTGCGCAAGCCCAAGGGCAAAAGATACAGCAGGGAGGCGCTGGAGATCTGTGCG	3245
Db	2935	GCTGTGCTGTATGCAACAAGGGCAAAAGATGGGCGGGGAGGCGCTGGAATCTTCAGT	2994
QY	3246	AAGATAGAAACAGAGAGATAGAGAGTCTGAACTTTGGAAAGCAATGTGACAGCATGAGACC	3305

Db	2995	GAGATTGTAACGAGAGATTGGAGTCTGAACTTGGAAAGCCAAATGTGTGACAGCAGATGGAGCC	3054
OY	3306	TTGGCCCATGGGAAGAGGACCTGGCCACTCTGAAAAAGTGAATGAGAGAAAGTGGAAAGGACG	3365
Db	3055	TTGGCCCATGGAAAAAGGAGCTGGCCCTCTCTGAAAGGTGAGTGAAGGAAAGTGGAAAGGAGAG	3114
OY	3366	CTGTCAAGGAAGAGAGCAGAGAGTTTGACATGTGATATGGACCGCAGTGCAGATGGTAAATGCA	3425
Db	3115	CTGGAAGAGGAAGAGCTGAGACTTTTGACACGAAATATGGATGTGACATGACATGATGTATTACA	3174
OY	3426	GAGGCCCAAGAGATTGAAACAGAGCCAGAAATCTGGAGTTACGATCCAGACACTC	3485
Db	3175	GAAACCCCGAAGAGTTGTATACCGAGAGCCAGAAAGCCTGGGGTTACAATCCAGACACTC	3234
OY	3486	AACACATTGGATGGATCTCTACACTTAATAGACCAAGCCTGGCACTGTGTGATGAAGAGAGG	3545
Db	3235	AACACATTAGAGGCGCTCTCTGCACTCTGATGTGAGCAGCGCTCTCAAGTGTAGATGAAGAGAGGG	3294
OY	3546	CTGATCTTTACTCGAGAGCAGAAAGCTTTTCCGAGCCAAAGACTCAGATCAACAGCCAGCTAAGG	3605
Db	3295	CTGGTCTTTACTCGAGAGCAGAAAGCTTTCCGAGCCAAAGCCAGATCAACAGCCAACTGGCG	3354
OY	3606	CCCTTTGATGTGAGAGCTGTGAAGAGAGAGGCGACATCGCAGAAAGGCGCACCTCCGTTTCTGTG	3665
Db	3355	CCCATGTATGTGAGAGCTGTGAAGAGAGGCGACGTAGCAGAGGGGCGCACCTCCATTTTCTGTG	3414
OY	3666	GAGACTGACATAGATGGGATTCGTGGCGTATGTGAAGAAACGTGGAGAAATCATGAGGACAAC	3725
Db	3415	GAGACAAAGCATAGATGGGATTTCTGGCTGTATGTGAAGAACTTGGAGAAACATTAGGAGACAAC	3474
OY	3726	CTGGCCCCGGGCTGCTACAATACCCAGAGCTTTGAGCAACAGTGAAGCTGCTTTAGAT	3785
Db	3475	CTGGCCCCAGGCTCTCAATACCCAGAGCTTTGAGCAACAGTGAAGCTGCTCAATAAATAT	3534
OY	3786	TTTCTCAACCAAGGTTCTTTGGGATTCAACACCAAGCTGCTTTAGAAATTTTCCA	3837
Db	3535	TTTCTCAACGTAGGTTCTTTGGGATTCAACAGTCTCAGAGGCTCGGAGCCCAATGTCA	3586

RESULT 9	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	BASE COUNT	ORIGIN
162750	162750	Sequence 14 from patent US 5660982.	162750	162750.1	GI:2480458	Unknown.	Unknown.	1 (bases 1 to 4316)	Trygvason, K., Kallunki, P. and Pyke, C.	Laminin chains: diagnostic uses	Patent: US 5660982-A 14 26-AUG-1997;	Location/Qualifiers	1158 a	1033 c
												1..4316	899 t	
												/organism="unknown"		

Query Match	Score 2726;	DB 6;	Length 4316;
1st Local Similarity	68.3%;		
	88.5%;	Pred. No. 0;	

[illegible][illegible]

Db 1212 GATTTCAGCCCGCCCTGCTCTGTGAGCCCGACACCCTGGGTTGAAAGTGTATATGTCC 1271
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QY 1472 TCCAGACACAGAGAGACTGTACTAGGGGATGAGAACCTTGACATCCCTGAGTGTCTGA 1531
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Db	3366	GGTTTGATACCGAGAGCCAGAAAGCTGGGGTTTACATCCAGACACACTCAACATTTAGA	3425
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VERSION	U43327.2	GI:18921413	
KEYWORDS			
SOURCE	Mus musculus.		
ORGANISM	Mus musculus.		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 5158)		
TITLE	Yamada,Y.		
JOURNAL	Direct Submission		
ADTHORS	Submitted (13-DEC-1995) Laboratory of Developmental Biology, National Institute of Dental Research, National Institutes of Health, 9000 Rockville Pike, Bethesda, MD 20892, USA		
TITLE	2 (bases 1 to 5158)		
ADTHORS	Sugiyama,S., Utani,A., Yamada,S., Kozak,C.A. and Yamada,Y.		
TITLE	Cloning and expression of the mouse lamlnln gamma 2 (B2t) chain, a subunit of epithelial cell lamlnln		
JOURNAL	Eur.J. Biochem. 228 (1), 120-128 (1995)		
MEDLINE	95188894		
PUBMED	7882992		
REFERENCE	3 (bases 1 to 5158)		
AUTHORS	Sasaki,T., Gohring,W., Mann,K., Brakebusch,C., Yamada,Y., Fassler,R. and Timl,R.		
TITLE	Short arm region of lamlnln-5 gamma2 chain: structure, mechanism of processing and binding to heparin and proteins		
JOURNAL	J. Mol. Biol. 314 (4), 751-763 (2001)		
MEDLINE	21592560		
PUBMED	11733994		
REFERENCE	4 (bases 1 to 5158)		
AUTHORS	Sasaki,T. and Yamada,Y.		
TITLE	Direct Submission		
JOURNAL	Submitted (26-FEB-2002) Laboratory of Developmental Biology, National Institute of Dental Research, National Institutes of Health, 9000 Rockville Pike, Bethesda, MD 20892, USA		
REMARK	Sequence update by submitter		
COMMENT	On Feb 26, 2002 this sequence version replaced gi:1151216.		
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gene			
CDS			

[illegible]

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Db	692	TTGGAAAGCGGTTTACAGAAAGCGGGGACCTGCAAAACTCCACTGTGCACAGCCGCAATCG	751
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QY	968	TCCTTGGGAATCCAAAGGTGAGCTACGGGCAAGCCTTATCTTTTACTACGTTGTGGATAG	1027
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QY	1148	CAGATTAAATGACATCCAAAGCAGTAATTGGAGCCCCCAGCTAAAGTACTTGTAGTATCG	1207
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QY	1568	CCGAGGCTGCAGAGCGCGTCCCTTCGCAATGAGGTTTACGCTGCTCCGTAAGCTTGAGAC	1627
Db	1408	CCGAGGCTGCAGAGCGCATGTCCCTGTACAAATGAGGTTTACGCTGTATGTAAGCTTGAGAC	1468
QY	1628	AGAGAGAGTGTGTGCATAATCACTGCCCCCAGAGGTGCTCACTGTGCCGCTGTGAGCTGTG	1687
Db	1468	AGAGAGAGTGTGTGTAAACAATGTCCCCCTGGGGTCAACAGTGTGCCCTGTGAGCTGTG	1528
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OY	1518	CCTGAGTGTGCTGACTGCCCATTTGTTTCTTACAACGATCCACAAGACCCCCGAGCTGC	1577
OY	1260	--TGATGTGTGCTGACTGCCCATTTGTTTCTTACAATGACCAATGACATGACCCCGAGCTGC	1317
OY	1578	AAGCCGTCGCCCTGTGCGATATGGGTTCACTGCTCCGTGATGCTGAGACAGAGAGGTG	1637
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OY	1638	GTCGTGACATATCTGCCCGAGGGGTACATGTCGCCGTGAGCTGTGATGATGAGG	1697
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OY	1438	TTCCTTTGGGGATCCCTTTGGGGAAACATGTGCCCATGTAGAGCTTGTGTCAACGCTGTCCAAATGC	1497
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Db	1498	AAACAACAAGTGGAGACCCCAATGGCTCTGGGAACTGTGCACAGTTGTACAGGAGCATGCTTG	1557
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Db	1918	CAGGCGCTCTTTCAGGACATTTCTGGGAGAGACTAGATTTAGAAAGGGGCATATAGAGCCGTT	1977
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Db	1978	GCTGTCCGGCTGGCCCAAGGCAAGGAGCCAGAGAAACGATCTCAAGAACCCGCTCGATGAC	2037
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Db	2278	CTAGCAAGGAGAACTGAGGAGTACTCTCCAAACAGACACTTTATTTTGGCCCGAAGCTCTTG	2337
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Dp	2578	CTCTCAAAACGTGTGGACCAAGCAAAAGGATGCATTACAGCGTGTGGCAAAACATCTGGGG	2637
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Dp	3415	ACTAGCATAGATGGGAATTTCTGTGATGTGAAGAACTGGGAGAACATTCGAGACAACTG	3474
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LOCUS					
DEFINITION	Mus musculus 100kDa nicotin (NICB2)		mRNA	sequence.	
ACCESSION	L20477				
VERSION	L20477.1	GI:833765			

KEYWORDS	laminin; nicein.
SOURCE	Mus musculus strain C57BL/C CDNA to mRNA.
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1393)
AUTHORS	Aberdam,D., Galliano,M.F., Mattel,M.G., Pisanì-Spadafora,A., Ortonne,J.P. and Meneguzzi,G. Assignment of mouse nicein genes to chromosomes 1 and 18 Mamm. Genome 5 (4), 229-233 (1994) 94281750
JOURNAL MEDLINE	8012114
PUBMED	2 (bases 1 to 1393)
REFERENCE	Aberdam,D., Aguzzi,A., Baudoin,C., Galliano,M.F., Ortonne,J.P. and Meneguzzi,G. Developmental expression of laminin adhesion protein (laminin-5) subunits suggests multiple morphogenic roles Cell Adhes. Commun. 2 (2), 115-129 (1994).
JOURNAL MEDLINE	94363405
PUBMED	8081888
REFERENCE	3 (bases 1 to 1393)
AUTHORS	Aberdam,D.
TITLE	Direct Submission
JOURNAL	Submitted (02-MAY-1994) Daniel Aberdam, Faculte de Medecine, INSERM U355, Ave de Valombrose 06107, Nice Cedex 2, France
COMMENT	On May 26, 1995 this sequence version replaced gi:476722;
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SOURCE	I..1393

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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauia; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 1 (bases 1 to 3020)
 Halfter, W., Dong, S., Balasubramani, M. and Bier, M.E.
 Aberrant histogenesis after temporary disruption of the retinal
 basal lamina
 JOURNAL
 Unpublished
 2 (bases 1 to 3020)
 Dong, S., Balasubramani, M., Halfter, W. and Bier, M.E.
 Direct Submission
 Submitted (26-APR-2001) Neurobiology, University of Pittsburgh,
 3500 Terrace Street, Pittsburgh, PA 15261, USA
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Job time : 10052 secs

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DR WPI: 1996-209366/21.
DR P-PSDB: AAR91427.
PT Detection of kalinin or laminin 5 expression in cells - useful to
PT detect, monitor and inhibit the invasive growth of cell in tissue,
PT partic. malignant tissue
PS Disclosure: Fig 4A; 37Pp; English.
XX The present sequence is the full cDNA (Genbank 215008) encoding the
CC kalinin/laminin 5 gamma-2 chain (R91427). The gamma-2 chain is of
CC importance to patients suffering from epidermolysis bullosa, esp. the
CC junctional form (JEB). Probes and antisense gamma-2 sequences derived
CC from this sequence can be used to detect, monitor and inhibit the
CC invasive growth of cells in tissue, partic. malignant tissue.
XX Sequence 5200 BP; 1364 A; 1236 C; 1392 G; 1208 T; 0 other;
Query Match 74.98; Score 2986.2; DB 17; Length 5200;
Best Local Similarity 88.58; Pred. No. 0;
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DB 14 AAGAAAAGAGAGACAGCGAGCGAGCGAGAGTGAACCTCCAGCGCGGGC 71
QY 159 AGCGACCCCTGCAGCGCGG-----GACCGCGCGCGCGCTGGCATGCTGCTCTG 211
DB 72 AGCGACCCCTGCAGCGAGAGAGACTGAGCGCGCGCGCGCGCATGCTGCTCTG 131
QY 212 GCTGAGTGTCTACCTCTGCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 271
DB 132 GCTGAGTGTCT 191
QY 272 GGAAGTGTGATTGCAAGCGAGAGTCCAGCACTGATGATGATGATGATGATGATGAT 331
DB 192 GGAAGTGTGATTGCAAGCGAGAGTCCAGCACTGATGATGATGATGATGATGATGAT 251
QY 332 ACAGACAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 391
DB 252 ACAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 311
QY 392 CGAGAGTGTGAGAGAGAGATTTTACGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 451
DB 312 CGAGAGTGTGAGAGAGAGATTTTACGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 371
QY 452 TTGTAACCTTAAGTGTCTCTTACGCGTGCATGATGATGATGATGATGATGATGATGAT 511
DB 372 TTGTAACCTTAAGTGTCTCTTACGCGTGCATGATGATGATGATGATGATGATGATGAT 431
QY 512 GCCAGTGTGACAGAGAGAGAGTGTGACGAGTGTGCGCGGCTTCCACACTCACTGA 571
DB 432 ACCAGTGTGACAGAGAGAGAGTGTGACGAGTGTGCGCGGCTTCCACACTCACTGA 491
QY 572 TGTGAGTGTGCGCCCAAGAGAGAGAGTGTGACGAGTGTGACGAGTGTGACGAGTGTG 631
DB 492 TGTGAGTGTGCGCCCAAGAGAGAGAGTGTGACGAGTGTGACGAGTGTGACGAGTGTG 551
QY 632 CATCTAGAGGCGCTGTGACTCAGGCGCTGTGCTGCAAGCGCGGCTGTCACTGAGAGCG 691
DB 552 CATCTAGAGGCGCTGTGACTCAGGCGCTGTGCTGCAAGCGCGGCTGTCACTGAGAGCG 611
QY 692 CTGTGATAGGTGTGACAGAGTACTATCACTGATGAGGAGAGAGAGAGAGAGAGAGAG 751
DB 612 CTGTGATAGGTGTGACAGAGTACTATCACTGATGAGGAGAGAGAGAGAGAGAGAGAG 671
QY 752 CCAGTGTGTGTGATGAGAGATTCGCGACAGTGTGAGAGAGAGAGAGAGAGAGAGAG 811
DB 672 CCAGTGTGTGTGATGAGAGATTCGCGACAGTGTGAGAGAGAGAGAGAGAGAGAGAG 731
QY 812 TAAATCATCTGCTGCTCATCAAGATGATGATGATGATGATGATGATGATGATGATGAT 871
DB 732 TAAATCATCTGCTGCTCATCAAGATGATGATGATGATGATGATGATGATGATGATGAT 791

QY 872 GTCTCTGCAAAAGCTCCAGTGTGTCACAGCGCATCGGATATATTAAGTCAACAGAG 931
DB 792 GTCTCTGCAAAAGCTCCAGTGTGTCACAGCGCATCGGATATATTAAGTCAACAGAG 851
QY 932 ATCAGACCTGTCTATTTTGTAGCTCTCGCAAAATTTCTTGGATATCAAGGTGAGCTA 991
DB 852 ACTATGATCCGTCTATTTTGTAGCTCTCGCAAAATTTCTTGGATATCAAGGTGAGCTA 911
QY 992 CGGCGAAAGCTATCTTTTGTAGCTCTCGGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 1051
DB 912 TGGGCAAGGCTCTCTTGTAGCTCTCGGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 971
QY 1052 TGACGTATCTGGAAGGTGCTGTGTAGAGTACAGAGTCCCTTGTAGAGAGAGAGAG 1111
DB 972 TGATGTGATCTGGAAGGTGCTGTGTAGAGTACAGAGTCCCTTGTAGAGAGAGAGAG 1031
QY 1112 GACACTGCTTGTGGGATTCACCAAGCTTACATTCATTAATGAACATCCAGAG 1171
DB 1032 GACACTGCTTGTGGGATTCACCAAGCTTACATTCATTAATGAACATCCAGAG 1091
QY 1172 TAAATGAGAGAGAGAGAGAGTATGATGATGATGATGATGATGATGATGATGATGAT 1231
DB 1092 TAAATGAGAGAGAGAGAGAGTATGATGATGATGATGATGATGATGATGATGATGAT 1151
QY 1232 CCGCGAGATCCAGCTACCTACGAGAGATACAGTACTGGGTACATTCAGAGCTT 1291
DB 1152 CCGCGAGATCCAGCTACCTACGAGAGATACAGTACTGGGTACATTCAGAGCTT 1211
QY 1292 GATTTCAG 1351
DB 1212 GATTTCAG 1271
QY 1352 TGTGCTACAAAGGAGAGTGTGCGAGATGATGATGATGATGATGATGATGATGATGAT 1411
DB 1272 TGTGCTACAAAGGAGAGTGTGCGAGATGATGATGATGATGATGATGATGATGATGAT 1331
QY 1412 CAGACTGGAGCTTTTGGACCTGTATTCATGATTAATGCAAGAGAGAGAGAGAGAG 1471
DB 1332 GAGACTGGAGCTTTTGGACCTGTATTCATGATTAATGCAAGAGAGAGAGAGAGAG 1391
QY 1472 TCCAGACAGAGAGAGAGTGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1531
DB 1392 TCCAGACAGAGAGAGAGTGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1448
QY 1532 CTGCCCCATGATGATTTTACAAAGATCCAAAGAGAGAGAGAGAGAGAGAGAGAGAG 1591
DB 1448 CTGCCCCATGATGATTTTACAAAGATCCAAAGAGAGAGAGAGAGAGAGAGAGAGAG 1508
QY 1592 TCGCAATGGGTGAGTGTCTCCGTGATGCTGTAGACAGAGAGAGAGAGAGAGAGAG 1651
DB 1508 TCGCAATGGGTGAGTGTCTCCGTGATGCTGTAGACAGAGAGAGAGAGAGAGAGAGAG 1568
QY 1652 CCCCCAGAGTGTACAGTGTGCGCGCTGTAGAGTGTGTGAGAGAGAGAGAGAGAG 1711
DB 1568 CCCCCAGAGTGTACAGTGTGCGCGCTGTAGAGTGTGTGAGAGAGAGAGAGAGAGAG 1628
QY 1712 CTTGCGGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1771
DB 1628 CTTGCGGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1688
QY 1772 CCCTAGTGTGCGGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1831
DB 1688 CCCTAGTGTGCGGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1748
QY 1832 CAGAGTGTGAGTGTGAG 1891
DB 1748 CAGAGTGTGAGTGTGAG 1808
QY 1892 CAATCCAGAGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1951
DB 1808 CAATCCAGAGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1868

1952 GTGTCGAAGTGTGATGAGGCTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGCTGTGAGCA 2011
1869 ATGTGCAAGTGTGAGGCTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGCTGTGAGCA 1928
2012 TGCAGGCTGTGAGGCTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGCTGTGAGCA 2071
1929 TGGAGCAATT--CAGCTGTGAGGCTTGTGTTGTCACAAAGGCTTGTGAGCTGTGAGCA 1985
2072 TATGACAGGCTGTGAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGCTGTGAGCA 2125
1986 TATGACAGGCTTGTGAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGCTGTGAGCA 2045
2126 AGTACCAAGGCTGTGAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGCTGTGAGCA 2185
2046 AGTACCTGTATGAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGCTGTGAGCA 2105
2186 TCTGAGGAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGCTTGTGAGCTGTGAGCA 2245
2106 TCTGAGGAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGCTTGTGAGCTGTGAGCA 2165
2246 GGCAGGCTTGTGAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGCTTGTGAGCA 2305
2166 GGTGAGGCTTGTGAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGCTTGTGAGCA 2225
2306 AAGAGTGTGAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGCTTGTGAGCTTGTGAGCA 2365
2226 AAGAGTGTGAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGCTTGTGAGCTTGTGAGCA 2285
2366 CACTGAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGGCTTGTGAGCTTGTGAGCA 2425
2286 CACTGAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGGCTTGTGAGCTTGTGAGCA 2345
2426 TCTGAGGAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGGCTTGTGAGCTTGTGAGCA 2485
2346 TGCCTGAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGGCTTGTGAGCTTGTGAGCA 2405
2486 ATTGAGGAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGGCTTGTGAGCTTGTGAGCA 2545
2406 ATTGAGGAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGGCTTGTGAGCTTGTGAGCA 2465
2546 GAGTATTTCCAAAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGGCTTGTGAGCTTGTGAGCA 2599
2466 GAGTATTTCCAAAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGGCTTGTGAGCTTGTGAGCA 2535
2600 CGGAGGAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGGCTTGTGAGCTTGTGAGCA 2659
2526 CGGAGGAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGGCTTGTGAGCTTGTGAGCA 2585
2660 TAAATCTGTGAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGGCTTGTGAGCTTGTGAGCA 2719
2586 CAAATCTGTGAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGGCTTGTGAGCTTGTGAGCA 2645
2720 GTCTTATGAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGGCTTGTGAGCTTGTGAGCA 2779
2646 GTCTTATGAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGGCTTGTGAGCTTGTGAGCA 2705
2780 TCAATCTGTGAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGGCTTGTGAGCTTGTGAGCA 2836
2706 TCAATCTGTGAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGGCTTGTGAGCTTGTGAGCA 2765
2837 CCGTGTGAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGGCTTGTGAGCTTGTGAGCA 2896
2766 CCGTGTGAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGGCTTGTGAGCTTGTGAGCA 2825
2897 AGAAGAAAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGGCTTGTGAGCTTGTGAGCA 2956
2826 AGAAGAAAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGGCTTGTGAGCTTGTGAGCA 2885
2957 GCTTCCGCTGCAAGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGGCTTGTGAGCTTGTGAGCA 3016
2886 GCTTCCGCTGCAAGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGGCTTGTGAGCTTGTGAGCA 2945
3017 CACTTTTATGAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGGCTTGTGAGCTTGTGAGCA 3076

2946 CACTTTTATGAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGGCTTGTGAGCTTGTGAGCA 3005
3077 AGTAAAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGGCTTGTGAGCTTGTGAGCA 3136
3006 CAAAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGGCTTGTGAGCTTGTGAGCA 3065
3137 TGCAGTGTGAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGGCTTGTGAGCTTGTGAGCA 3196
3066 TGCAGTGTGAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGGCTTGTGAGCTTGTGAGCA 3125
3197 CGCCAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGGCTTGTGAGCTTGTGAGCA 3256
3126 TGCAGAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGGCTTGTGAGCTTGTGAGCA 3185
3257 GAGATGAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGGCTTGTGAGCTTGTGAGCA 3316
3186 GAGATGAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGGCTTGTGAGCTTGTGAGCA 3245
3317 GAGAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGGCTTGTGAGCTTGTGAGCA 3376
3246 AAGAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGGCTTGTGAGCTTGTGAGCA 3305
3377 GAGAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGGCTTGTGAGCTTGTGAGCA 3436
3306 GAGAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGGCTTGTGAGCTTGTGAGCA 3365
3437 AGTAAAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGGCTTGTGAGCTTGTGAGCA 3496
3366 GGTGATGAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGGCTTGTGAGCTTGTGAGCA 3425
3497 TGCAGTGTGAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGGCTTGTGAGCTTGTGAGCA 3556
3426 CGGCTGTGAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGGCTTGTGAGCTTGTGAGCA 3485
3557 GAGAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGGCTTGTGAGCTTGTGAGCA 3616
3486 GAGAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGGCTTGTGAGCTTGTGAGCA 3545
3617 AGAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGGCTTGTGAGCTTGTGAGCA 3676
3677 AGATGAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGGCTTGTGAGCTTGTGAGCA 3736
3606 AGATGAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGGCTTGTGAGCTTGTGAGCA 3665
3737 CTGCTAAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGGCTTGTGAGCTTGTGAGCA 3796
3666 CTGCTAAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGGCTTGTGAGCTTGTGAGCA 3725
3797 GGTCTGTGAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGGCTTGTGAGCTTGTGAGCA 3837
3726 GGTCTGTGAGGCTTGTGTTGTCACAAAGGCTTGTGAGGCTTGTGAGGCTTGTGAGCTTGTGAGCA 3766

RESULT 2
AAC83729
ID AAC83729 standard; cDNA: 5200 BP.
AAC83729:
02-MAR-2001 (first entry)
DE Human laminin 5 cDNA, SEQ ID NO: 25.
XX Human laminin 5 cDNA, SEQ ID NO: 25.
AC Human laminin 5 cDNA, SEQ ID NO: 25.
XX Human laminin 5 cDNA, SEQ ID NO: 25.
RW Human laminin 5 cDNA, SEQ ID NO: 25.
KW Human laminin 5 cDNA, SEQ ID NO: 25.
OS Homo sapiens.
XX Homo sapiens.
PN WO200066731-A2.

XX	09-NOV-2000.
PD	
XX	
XX	28-APR-2000; 2000MO-US11459.
PF	
PR	30-APR-1999; 99US-0131720.
PR	21-AUG-1999; 99US-0149738.
PR	24-SEP-1999; 99US-0155945.
XX	
PA	(BIOS-) BIOSTATUM INC.
PI	Boutaud A:
XX	
XX	WPI, 2000-687538/67.
DR	P-PSDB; AAB48468.
XX	
PT	laminin 5-expressing cells, used to accelerate wound healing associated
PT	with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
XX	burns, acute wounds and skin grafts -
XX	
PS	Claim 4; Page 175-181; 232pp; English.
XX	
CC	The present sequence encodes a laminin 5 chain polypeptide. Recombinant
CC	laminin 5-expressing cells are used to accelerate wound healing,
CC	especially diabetic foot ulcers, venous ulcers, pressure sores, skin
CC	surgery, burns, acute wounds, skin grafts, corneal ulcerations,
CC	gastro-intestinal ulcers, periodontitis, and gingivitis. They are also
CC	used to improve the biocompatibility of medical devices, and to promote
CC	cell adhesion to a surface. They can be used for the ex vivo treatment
CC	of type I diabetes. Laminin can also be used to regulate angiogenesis.
CC	The cell line produces and secretes recombinant heterotrimeric laminin,
CC	whereas prior art cell lines have been created that produce but do not
CC	secreted only one or two chain laminins.
XX	
SQ	Sequence 5200 BP; 1364 A; 1236 C; 1392 G; 1208 T; 0 other;
	Query Match 74.9%; Score 2986.2; DB 21; Length 5200;
	Best Local Similarity 88.5%; Pred. No. 0;
	Matches 3328; Conservative 0; Mismatches 403; Indels 30; Gaps 7
QY	99 AAGGAAAAAGGAAGGCACAGCGCAGAGTGAGAATCTCCAGCGGGCGGCCGGCC 158
DB	14 AAGGAAAAAGGAAGGCACAGCGCAGAGTAGAAGAACCAACCAC--CGAGCGCGCGGC 71
QY	159 AGCGACCCCTGCGAGGGG-----GAACGGGGCGCGGCCGCGCATGCGGCTCTG 211
DB	72 AGCGACCCCTGCGAGGGGAGACAGAGACTGAGGCGGCCCGCACCGCATGCTGCGCTTG 131
QY	212 GCTGAGCTGTACTCTCTGCTTCTCGCTCTCTCTGCGCGAGCGCGGCGACCTCCGGAG 271
DB	132 GCTGGCGTGTGCTCTCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 191
QY	272 GGAAGTCGTGATTGCCAAAGGGAGTCCAGGCATGATCTTTGACCAAGAACTTCACA 331
DB	192 GGAACTGTGTATTCATATGGGAATCCAGGCAAGTATCTTTGATCGGAATTCACAG 251
QY	332 ACAGACAGAAATGGATTCGCTGCTCAACTGCAATGACATGATGATGATGATGATGATG 391
DB	252 ACAAACTGTATATGGATTTCGCTGCTCAACTGCAATGACATGATGATGATGATGATGATG 311
QY	392 CGAGAGTGTCAAGCGAGATTTTACCGACAGAGAGAAAAGGACCGCTGTTTACCTGCA 451
DB	312 CGAGAGTGTCAAGAGATGGCTTTTACCGGACAGAGAAAAGGACCGCTGTTTCCCTGCA 371
QY	452 TTGTACTCTTAAGGTTCTTTAGCGCTGATGTGACAACTCTGAGCGGTGAGCTGTAA 511
DB	372 TTGTACTCTCAAAGGTTCTTTAGGCTGATGTGACAACTCTGAGCGGTGAGCTGTAA 431
QY	512 GCCAGCTGTGACAGAGACAGTGTGACCGAGTGTGCCCCGCTTCCACACACTACATA 571
DB	432 ACCAGTGTGACAGGACGACATGTGGACCGAGTGTGCGACGCTTCCACATCTCCAGA 491
QY	572 TGCTGGGTGCGCCCAAGACCAAAGGCTGTATATCTTCAAGTGTGACTGTGACCTAGCTGG 631

Db	492	TGCGGGGTGACCCCAAGACAGAGACTGCTAGACTCCAAAGTGATGACTGTGACCCAGCTGG	551
QY	632	CATCTCAGAGGCCCTGTGACTCAGAGCGCGGTGTGTGCAAGCGCGGCTGTCACTGGAGACG	691
Db	552	CATCCACAGGGCCCTGTGACGCGGGCCGCTGTGTCTGCAAGCCAGCTGTACTGGAGAACG	611
QY	692	CTGTGATAGTGTGACACAGGTGTACTATCACCTGGATGGGGGAAACCTCAGGGCTGTAC	751
Db	612	CTGTGATAGTGTGATCAGAGTGTACTATTAATCTGGATGGGGGAAACCTGAGGGCTGTAC	671
QY	732	CCAGTGTTTTGTCTATGGGCATTTCCGCCAGCTGCCACAGCTCTGGGGACTACATGTGTCA	811
Db	672	CCAGTGTTCCTATGTGGGCATTTCCAGCAGCTGCCGACGCTGTGAGATACAGTGTCTCA	731
QY	812	TAAATATCATCTGTGCTTCCTCCATCAAGATGTGTGATGGCGGAAGGCTGCCAAAGAAAGG	871
Db	732	TAAATATCACTCTTACTCTTATCATCAAGATGTGTGATGGCGGAAGGCTGCCAAAGAAAGG	791
QY	872	GTCCTCTCCAAAGCTCCAGTGGTCCACAGCGGCATCGGAGTATATTTTACTCAGCAGCAG	931
Db	792	GTCCTCTCCAAAGCTCCCAATGGTCCACAGCGGCATCAAGATGTGTGTACTCAGCAGCAG	851
QY	932	ATCAGACCCCTGTCTATTTTGTAGCTCTGCCAAATTTCTTGGGAATCAACAGGTGAGCTA	991
Db	852	ACTAATATCCTGTCTATTTTGTAGCTCTGCCAAATTTCTTGGGAATCAACAGGTGAGCTA	911
QY	992	CGGGCAAGGCCATATCTTTTGTACTACCGGTGGATGGGGAGGACAGACCCATCTGCCCA	1051
Db	912	TGGGCAAGGCCGTCTCTTGTAGCTACCGGTGGATGGGGAGGACAGACCCATCTGCCCA	971
QY	1052	TGACGTGATCCTGGAAGGTGCTGTGCTACGGATCAACAGCTCCCTGTGATGCCACTTGCAA	1111
Db	972	TGATGTGATCCTGGAAGGTGCTGTGCTACGGATCAACAGCTCCCTGTGATGCCACTTGCAA	1031
QY	1112	GACACTGCTTGTGGGATCCACAGACTTACACATTCAGATTAAATGAACATCCACAGCAG	1171
Db	1032	GACACTGCTTGTGGGCTCACCAGACTTACACATTCAGATTAAATGAACATCCACAGCAA	1091
QY	1172	TAAATGGAGCCCCCAGCTAAGTTCCTTGAGATTCGGAGGTTTACGGGGAACCTCAGCAGC	1231
Db	1092	TAAATGGAGCCCCCAGCTGAGTACTTGTAGATTCGAAGGTTTACTGGCGAATCTCAGCAGC	1151
QY	1232	CTCGGGATCCGAGCTTACCTACGAGAAATACAGTACTGGGTACATTGCAACGTAACCTT	1291
Db	1152	CTCGGGATCCGAGCTTACATATGGAAGATACAGTACTGGGTACATTGCAATGTGACCTT	1211
QY	1292	GATTTTCAGCCCGCCGTTTCTGAGCCCCCAGCGCCCTGGGTTGAACATGTGTATGCC	1351
Db	1212	GATTTTCAGCCCGCCCTGTCTGTGGAGCCCCCAGCACCCTGGGTTGAACATGTATATGCC	1271
QY	1352	TGTTGGGTACAAAGGGGCACTTCGCCAGAGATTTGGCTTCGGGCTTCACAAAGAGATTCAGC	1411
Db	1272	TGTTGGGTACAAAGGGGCAATTCGCCAGAGATTTGGCTTCGGCTTCACAAAGAGATTCAGC	1331
QY	1412	CAGACTGGGACCTTTTGGCACCTGTATTCATGTAACTGCCAAAGGGGAGGGGCTCTGCA	1471
Db	1332	GAGACTGGGACCTTTTGGCACCTGTATTCATGTAACTGTCAAGGGGAGGGGCTCTGCA	1391
QY	1472	TCCAGACACAGAGACTGTCTACTCAGGGGATGAGAACCTTGACATCCTTGAGTGTCTGA	1531
Db	1392	TCCAGACACAGAGAGATGTCTATTCAGGGGATGAGAACCTTGACATCCTTGAGTGTCTGA	1448
QY	1532	CTGGCCCCATGGTTTCTCAACAAGATCCCAAGACCCCGGACAGCGTCGACCCCTCTG	1591
Db	1449	CTGGCCCCATGGTTTCTCAACAAGATCCGACAGACCCCGGACAGCTGCAAGCCATGTCCCTG	1508
QY	1592	TCCGATATGGTTCAGACTCTCCGTGATCCTGAGACAGAGAGAGGTGTGTCAATTAATG	1651
Db	1509	TCCATACAGGTTTCAGACTCTCAGTATTCGGAAGACGAGAGAGGTGTGTCAATTAATG	1568
QY	1652	CCCCCAGGGTGTCACTGGTCCCGCTGTGAGCTCTGTGCTATGAGCTATTTTGGGACCC	1711

Dp	1569	CCCTCCCGGGGTCAACCGGTCGCCCGCTGTAGACTCTGTGCTGATGAGCTACTTTTGGGACCC	1628
Oy	1712	CTTCGGGGAAACGTGGCCCACTAGAGCCCTTGTCAAGCCTGTCACTGCAACAACAACGTGA	1771
Dp	1629	CTTTGGTGAACATGTCGCCCACTGAGAGCCTTGTACAGCCCTGTCAATGCAAACAGCAATGGGA	1688
Oy	1772	CCCTAGTGCCTCCGGGAACTGTGACCCGCTGACAGGCAAGTGTCTGAATGCATCCACAA	1831
Dp	1689	CCCCAGTGCCTCTGGGAAATTGTGACCCGCTGACAGGCAAGGTGTTTGAAGTGTATCCCAA	1748
Oy	1832	CACAGCTGGGGTCCACTGTGACCCAGTGCAAAGCAGGCTACTATGAGGGGACCCGTTGGCTCC	1891
Dp	1749	CACAGCCGCGCTTACTTCTCGACAGTGCAAAGCAGGCTACTTGGGGAACCATTTGGCTCC	1808
Oy	1892	CAATCCAGCAGACAAGTGTGAGCTTCAACTGCACCCAGTGGGCTCGGAGCCTGTGA	1951
Dp	1809	CAACCCAGCAGACAAGTGTGAGCTTCAACTGTAAACCCATGGGCTCAGAGCCTGTAGG	1868
Oy	1952	GTGTCCAAAGTATGCGACGTGTGTTTCCAAAGCCAGGCTTTGTGTGCTCAAGTGTGACA	2011
Dp	1869	ATGTCCGAAGTATGTGCGACCTGTGTTTCCAAAGCCAGGATTTGTGTGGCCCCCAACTGTGACA	1928
Oy	2012	TGGGCGACTGCACCGAGCTGCAGCTTCTTAATCAAGTAAAGTTTCAAGTGTGATCGTT	2071
Dp	1929	TGAGCACTT---CAGCTGTCCAGCTTCTTAATCAAGTAAAGTTTCAAGTGTGATCGTT	1985
Oy	2072	TATGCACAGCTCCAGATCTCTGAGAGCCCTGTGATTTCCAAAGCCTCAGGG-----TGAGC	2125
Dp	1986	TATGCACAGCTTCCAGAGAAATGAGAGCCGATTTTCAAAGGCTCAGGGTGGTATGTGAGT	2045
Oy	2126	AGTACCCAACGCAAGCTGGAAGGCAAGATGACAGAGCTGTAGCAGGCCCCCTTGGGACAT	2185
Dp	2046	AGTACCTGATTCACAAGCTGTGGAAGGCAAGATGACAGAGCTGTAGCAGGCCCCCTTCAAGACAT	2105
Oy	2186	TCTAGAGAAGCCCGAGATTCACAAGATGCGTGTAGATTCCTTCAATCTCGGGGGGCGCAA	2245
Dp	2106	TCTAGAGATGTCCCGAGATTTCTAGAAGGTGTGCTAGCAGATTCCTTGTGTCTTCCAGTTGGCCAA	2165
Oy	2246	GGCAAGGACCTCAGAGATATAGCTACCGGAGCCGCTGTGATGACCTCAAGATGACTGTGA	2305
Dp	2166	GGTAGGAGGCCAAGAAAGACAGCTACAGAGCCGCTGGATGACCTCAAGATGACTGTGGA	2225
Oy	2306	AAGAGTTTGGGCCCTGGGCACTGATTCAGAACCAAGTTCAAGATCTCGCAGGCTCAT	2365
Dp	2226	AAGAGTTTGGGCTCTGGGAAGTCAAGTACAGAAACCGAGTTGCGGATCTCTCACAGAGCTCAT	2285
Oy	2366	CACACAGATGGCCCTGAGGCGTGGAGGAAAGTGAAGGCTCCCTGCAAAACCAACATTC	2425
Dp	2286	CACACAGATGTGAGTGAAGCTGGCGAAGAAAGTGAAGCTTCTTTGGGAAACCAATTCATTC	2345
Oy	2426	TCTCTTCAGAGACTACGTTGGGCGCAAAATGCTTTAAAGTGTGCTCAGAGAGCCACGAG	2485
Dp	2346	TGCTCTGAGACACTACGTTGGGCGCAAAATGCTTTAAAGTGTGCTCAGAGAGCCACAG	2405
Oy	2486	ATTGGCAGACAGCCATGTTCAGTACGCCAGTTAACATGAGAGCACTGGCAAGAACCA	2545
Dp	2406	ATTGACAGAAAGCCACGTTGATGACGCAGTAACATGGAGCAACTGCACAAAGGAACTGA	2465
Oy	2546	GGACTATTTCACAAAGAGCTGTACGTGTCGGAAGGCCCCCTGTGATTAAGGATGCGAGG	2599
Dp	2466	GGACTATTTCACAAAGAGCCCTCTTCACTGTGTGCGGAAGGCCCCCTGTGATTAAGGATGCGAGG	2525
Oy	2600	CGGAAGCGGCGCCTGAGCGAGGCGCGTGGTSCAAAGGCTTTGGGAAAAATTTGCGAAAC	2659
Dp	2526	CGGAAGCGGTATGCCCGGACGCTGTGTGTGTCAAAGGCTTTGTGAAAAATTTGCGAANAAC	2585
Oy	2660	TAAATCTCTGGCCCAAGAGTGTGCAAGGAGGCCACGCAACACGACATGGAAGCAGATAG	2719
Dp	2586	CAAGTCCCTGGCCAGCAGTTGACAAGGAGGCCATCCACGGAATTTGAAGCAGATAG	2645
Oy	2720	GTCTTATCAGATATGTCTCCACCTTTCTCAATTTCCGTGTCTAGATTCAGGAGTCAATGA	2779
Dp	2646	GTCTTATCAGACAGTCTCCGCTCTCTCTGTGATGATGTCTCCGCTGTAGGAGTCAAGTA	2705

QY	2780	TCAGTCTCTGCAAGT---AGAGGCAAGAGGCTCAGACAAAAAAGCTATTTCTCTCAAA	2836
Db	2706	TCAGTCTCTTTCAGGTGGAAAGGCAAAAGAGATCAAAACAAAAACGGATTTCACCTCAAG	2765
QY	2837	CCGATGACACTAAGCATATGATAGATTCAAGCTCAACGACGTGCAAAAGCATCTGGGAAACTGGGA	2896
Db	2766	CTCGGTAAACCAAGCATATGATATGATGTTCAAGCTACACAAAAAGAAATCTGGAAACTGGAA	2825
QY	2897	AGAGAAACC CGGAGCTCTTACAGAAATGGAAGAAATGGGAGACAGACATTCAGATCAAGCTY	2956
Db	2826	AGAGAAAGACACAGAGCTCTTACAGAAATGGAAGAAAGGGGAGAGAGAAATTCAGATCAAGCT	2885
QY	2957	GCTTCCCGTCCCAACCTTGGTAAAGCAGAGCCCAAGAAAGCAGTAAATGATTTGGCATTGCG	3016
Db	2886	GCTTCCCGTCCCAATCTTGGTAAAGCAGAGCCCAAGAAAGCAGTAAATGATTTGGCATTGCG	2945
QY	3017	CACATTTTATGAAGTTGAGAACATCTTAAAGAAATCTCAGAGAGTTTGACCTGCAAGTTGG	3076
Db	2946	CACATTTTATGAAGTTGAGAACATCTTAAAGAAATCTCAGAGAGTTTGACCTGCAAGTTGG	3005
QY	3077	AGATTAAGAACACAAAGCTGGAAGAGCCATTAAGAGACTCTCTTACATTCAGCCAGAAAGCT	3136
Db	3006	CAACAGAAAGAACAGAGCTGGAAGAGCCATTAAGAGACTCTCTTACATTCAGCCAGAAAGCT	3065
QY	3137	TGCAGGTGCCAGTATACAAAGAGAAAGCAAGCAGAGCAGCCCTGGGCGAGTGTGCTGCCGA	3196
Db	3066	TTCAGATGCCAGTGCACAAAGCCACAGCAAGCAAGAAAGCCCTGGGAGCGCTGTGCTGCA	3125
QY	3197	CGCCCAAGGCGCAAAAGATTCAGCCAGGAGGAGCCCTGGAGATCTCTGGCAAGATAGAACCA	3256
Db	3126	TGCACAGAGGCGCAAAAGATTCAGGAGGAGGAGCCCTGGAAATCTCAGATGAGATTGAACA	3185
QY	3257	GGAGATAGAGAGTGTGAACCTTGAAAGCCAAATGTGACAGCAGATGAGAGCTTGGCCATGGA	3316
Db	3186	GGAGATTTGGAGTGTGAACCTTGAAAGCCAAATGTGACAGCAGATGAGAGCTTGGCCATGGA	3245
QY	3317	GAAAGGAGTGGCCACTCTGAAAAGTGAAGATGAGAGAGAGAGTGGAAAGAGAGCTGTCAAGGAA	3376
Db	3246	AAAAGGAGTGGCCCTCTCTGAAAGAGTGAAGTGAAGGAAAGTGGAAAGAGAGCTGTCAAGGAA	3305
QY	3377	GGAGAGAGAGTTTGATGATGATGATGGAAGCAGAGTGCAGATGGTAAATTCAGAGGCCCAAG	3436
Db	3306	GGAGCTGAGTTTGATGATGATGATGGAAGCAGAGTGCAGATGGTAAATTCAGAGAGGCCCAAG	3365
QY	3437	AGTTGAAAACAGAGCCAGAAATGCTGAGATTACGATCCAGACACACTCAACACATTGGA	3496
Db	3366	GTTGATACCAAGAGCCAGAACCGCTGGGTTACATTCAGAACACACTCAACACATTGGA	3425
QY	3497	TGGCATCTCAACCTTAATAGACAGAGCTGGCAGATGTGATGAATGAAGAGAGCTGATCTTACT	3556
Db	3426	CGGCTCTCTGATCTGATGAGACACAGCCCTCAAGTGTAAATGAAGAGAGGAGCTGATCTTACT	3485
QY	3557	GGAGCAGAGAGCTTTTCCAGGCCAAGACACTCAGATCAACAGCCAGCTACAGCCCTTGATGTC	3616
Db	3486	GGAGCAGAGAGCTTTTCCAGGCCAAGACACTCAGATCAACAGCCAGCTACAGCCCTTGATGTC	3545
QY	3617	AGATGGAGATTCAGGCTGATGTGAAGAACCTGGAGAAATCAAGGGGCAACCTGGCCCCGGG	3736
Db	3606	AGATGGAGATTCAGGCTGATGTGAAGAACCTGGAGAACCTTGAAGAACCTTGAAGAACCTGGCCCCG	3666
QY	3737	CTGCTACAAATACCCAGGCTCTTGAGCAACAGTGAAGCTCCCTTAGAGATTTCTCAACCAA	3796
Db	3666	CTGCTACAAATACCCAGGCTCTTGAGCAACAGTGAAGCTCCCATTAATATTTCTCAACTGA	3725
QY	3797	GATTCTTGGGATTCAGACCTAGCTGCTTAAAGATTTCTCA	3837
Db	3726	GATTCTTGGGATTCAGATCTCAGGCTCGGGAGCCCATATCA	3766

OY	1232	CCTCGGAGTCCGAGCTACCTACGAGAAATACAGTACTGGGTACTTATGACAACGTGACCTT	1291
Db	1152	CCTCCGGATCCGAGCTACATATGGAAGATACAGTACTGGGTACTTATGACAATGTGACCTT	1211
OY	1292	GATTTCAGGCCGCCCTGTTCTGGAGGCCAGGCCCTGGGGTTAAACAATGTGATGCC	1351
Db	1212	GATTTCAGGCCGCCCTGTCTCTGGAGGCCAGGCCCTGGGGTTAAACAATGTATATGTCC	1271
OY	1352	TGTTGGCTACAAGGGGAGTTCCTGCCAGGATTTGCTTCCGGCTCAAAAAGAGATTGACG	1411
Db	1272	TGTTGGGTACAAGGGGCAATTCTGCAAGGATTTGCTTGGGCTACAAGAGATTGACG	1331
OY	1412	CAGACTGGGACCTTTTGGCACCTGTATTTCCATGTATACGCCAGGGGAGGGGCTCGCA	1471
Db	1332	GAGACTGGGGGCTTTTGGCACCTGTATTTCTTTACTGTCTCAAGGGGAGGGGCTCTGTA	1391
OY	1472	TCCAGACACAGAGACACTGTACTATAGGGGAATGAACCCGTACACTCCCTGAGTGTGTA	1531
Db	1392	TCCAGACACAGAGAAATTTGTTATTCAGGGGATGAGAAATCTGACAT---TGAGTGTGTA	1448
OY	1532	CTGCCCCATTGGTTTTCACAACGATTCACAAGACCCCCGACGCTGCAAGCGCTGCCCTG	1591
Db	1449	CTGCCCAATTGGTTTTCACAACGATTCGACAGACCCCCGACGCTGCAAGCGATGTCCCTG	1508
OY	1592	TCCGAATGGGTTCAGCTGCTCTCCGTGATGCTTGAGACAGAGAGAGTGTGTCAATTAAGT	1651
Db	1509	TCATTAAGGGGTTTCAGCTGCTCTCAGTAATTCGGAACACGGAGAGGTGTGTGCAATTAAGT	1568
OY	1652	CCCCCAGGTTTCACGTGGTCCGCTGTGACCTCTGTGCTGATGGCATTTTGGGGAGCC	1711
Db	1569	CCCTCCGGGGTACACGGTGCCTGCTGACCTCTGTGCTGATGGCTACTTTGGGGAGCC	1628
OY	1712	CTTCCGGGAAAGTGGGCCAGTGAAGGACCTTGTACACCCCTGTGTCAGTCAACAACAGTGA	1771
Db	1629	CTTTGGTGAACATGTGGCCAGTGAAGGACCTTGTACACCCCTGTCAATGCAACAGCAATGTGA	1688
OY	1772	CCCTAAGTCCCTCCGGGAATGTGTGACCGCCTGACAGGAGGTGTCTGAAGTGCATCCAA	1831
Db	1689	CCCCAGTGCCCTCTGGGAATTTGTGACCGGCTGACAGCAGGTTTGAAGTGTATCCAA	1748
OY	1832	CACAGCTGGGGTCCACTGTGTACAGTGTGCAAGCAGGCTACTATGGGGACCCGTTGGCTCC	1891
Db	1749	CACAGCCGGCACTACTGTGACGACAGTGCAAAGCAGGCTACTTCCGGGACCCATTGGCTCC	1808
OY	1892	CATTCACAGACACAAGTGTGCAAGCTTGCACTGCAACCCAGTGGGCTCGAGACCTGTGA	1951
Db	1809	CAACCACAGACACAAGTGTGAGAGTTGTCACTGTAAACCCCATGGGCTCAGAGACCTGTAGG	1868
OY	1952	GTGTGCAAGTGTGGCAGCTGTGTTTTCACAGCCAGGCTTGGTGGCCTCAGCTGTGACA	2011
Db	1869	ATGTGCAAGTGTGGCAGCTGTGTTTTCACAGCCAGGATTTGGTGGCCCACTGTGACA	1928
OY	2012	TGCGGCATGACCAAGCTGTCCAGCTTGTATATCAAGTGAAGTTCAAGATGATCACTT	2071
Db	1929	TGAGGCAATT---CAGCTGTCCAGCTTGTCTATAATCAAGTGAAGTTCAAGATGATCACTT	1985
OY	2072	TATCAGAGAGCTCCAGATCCTGGAAGGCCCTATTTTCAAGGCTCAGAGG-----TGAGC	2125
Db	1986	TATGCAAGAGCTTTCAGAGATGGAAGGCCCTTATTTCAAGGCTCAGAGGCTGTATGGAGT	2045
OY	2126	AGTACCCACAAGCAGAGCTGGAAGGCAGAGATGACAGAGGCTGAGCAGAGGCCCTTCGGGACAT	2185
Db	2046	AGTACCTGATACAGAGGCTGAAGAGCAGGATGACAGAGGCTGAGCAGAGGCCCTTCAGAGCAT	2105
OY	2186	TCTGAGAGAACCCAGATTTTACAAGATGCTGTTAGATCTTCAATCTCCGGGTGGCCAA	2245
Db	2106	TCTGAGAGATCCCAAGATTTTCAGAGGCTGATGAGATCCCTTGCTCTCCAGTTGGCCAA	2165
OY	2246	GGCAAGAGCTCAAGAGATTAAGTCCGGGACCGGCTGGATATACCTCAAGATGACTGTGA	2305
Db	2166	GGTGAAGAGCCAAAGAACAGCTTACAGAGCGGCTGGATGATCTCAAGATGACTGTGA	2225
OY	2306	AAGAGTTCCGGCCCTGGGCACTGATGATACAGAACAGTTTACGATACTCGACAGCTCAT	2365

[illegible]

Db	847	AACAGGTAAGCTATGATGCTCAAAAGCCTGTCTTGA	CTACCTACCGTGTGACAGAGAGGACGAC	906
QY	1039	ACCACATCTGCCCACAGCGTGAATCTCTGGAAAGGTGCTGTCTAC	AGGATACAGGATCACAGCTCCCTTGA	1098
Db	907	ACCACATCTGCCCATGATGATGTGTTGGAAAGGTGCTGTCTAC	AGGATCACAGCTCCCTTGA	966
QY	1099	TGCCACTTTCAGCAGACACACTGCGCTGTGGGATACCAAGACTT	TACATTCAGATTTAAATG	1158
Db	967	TGCCACTTTCGCAACACACTGCGCTGTGGGCTCACCAAGACTT	CACATTCAGATTTAAATG	1026
QY	1159	AACATTCGAAGAGTAATTTGGAGGCCCCAGCTGAATTTACTT	CTGACTATCCGAGGTACTGC	1218
Db	1027	AGCATTCGAAGAAATTTGGAGGCCCCAGCTGAATTTACTT	CTGACTATCCGAGGTACTGC	1086
QY	1219	GGAATCTCACAGCCCTGGGATCCGAGCTACCTTCGGAAGATTA	CACTACAGTACAGTGGACATTTG	1278
Db	1087	GGATCTTCACAGCCCTCGCATCCGAGCTACATATGGAGAA	TACAGTACAGTGGACATTTG	1146
QY	1279	ACAAGTGAACCTTGATTTTCAAGCCGCCCGCTTTCTGGAAG	CCCCAGCCCGCCCTGGGTTTAAAC	1338
Db	1147	ACATGTGACCCCTGATTTTCAACCCGCCCGCTCTCTGGAG	CCCCAGCACCCCTGGGTTTAAAC	1206
QY	1339	AATGTGTATGCCCTCTGTTGGCTACAAAGGGGACGTTCTGC	CAGAGATTGTGCTTCGGGCTTACA	1398
Db	1207	AGTGTATATGCTCTGTTGGGTACAAAGGGGCAATTCGC	CAGAGATTGTGCTTCGGGCTTACA	1266
QY	1399	AAAGAGATTCAGCCAGACTGGGACCTTTTGGACCTGTGATTC	CAATGTAACGTCCAAAGGG	1458
Db	1267	AGAGAGATTCAGCCAGACTGGGACCTTTTGGACCTGTGATTC	CAATGTAACGTCCAAAGGG	1326
QY	1459	GAGGGGCCCTGGCATTCACAGACACAGAGAGACTTTTACT	CAGGGGATGAGAAACCTGCATATCC	1518
Db	1327	GAGGGGCCCTGGCATTCACAGACACAGAGAGATTGTATT	TCAGGGGATGAGAAATCTCAAT -	1384
QY	1519	CTGAGTGTGCTGACTGCGCCCATTTGGTTCTTACAACGAT	CACAAGACCCCGCAGCTTGA	1578
Db	1385	-TGAAGTGTGCTGAGCTGCCCAATTTGGTTCTTACAACGAT	CTCCGACAGACCCCGCAGCTTGA	1443
QY	1579	AGCGGTGGCCCTGTGCGAATGGGTTTACGCTCTCCGATGAT	CCGAGACACAGAGAGGTGG	1638
Db	1444	AGCATATGCCCTGTGATTAACCGGGTTACGGTCTACGTCT	CTCAGATATCCCGAGACGGAGAGGTGG	1503
QY	1639	TGTGCATTAATCTGCCCCCGAGGGTCTCACTGTGTGCCG	CTGTGAGCTCTGTGCTATATGGCT	1698
Db	1504	TGTGCATTAATCTGCCCTCCCGGGGTCAACGGTGTGCCG	CTGTGAGCTCTGTGCTATATGGCT	1563
QY	1699	ATTTTGGGGACCCCTGTGGGGACAGGTGGCCAGTGAAGG	CTTTGTACGCCCTGTCACTGA	1758
Db	1564	ACTTTGGGGACCCCTTGTGTGTAATATGGCCCAAGTAGAG	CCCTTGTTCAGGCCCTGTCAATGA	1623
QY	1759	ACAACAACGTGTGAACCTTAATGTGCTCCCGGGAACGTG	AACCGGCTACAGGGCAGGTGTGCA	1818
Db	1624	ACAACAATGTGTGAACCCCAAGTGCCTCTGTGGAAATTT	GTGACCGGCTACAGGGCAGGTGTGGA	1683
QY	1819	AGTGCATTCACAAACACAGCTGGGGTCTCACTGTGACCA	GTGCAAAAGCAGGCTACTATGGGG	1878
Db	1684	AGTGTATTCACAAACACAGCCGGGCAATCTACTCGACAC	AGTGTGCAAAAGCAGGCTACTTGGGG	1743
QY	1879	ACCCTGTGGCTCCCAATTCACAGACACAAGTGTGAAGT	TGCACTTGCACACCCAGTGGGCT	1938
Db	1744	ACCCTATGGGCTCCCAACCCACAGACACAAGTGTGCAAG	CTTGTCAACTGTAAACCCATGGGCT	1803
QY	1939	CGGAGCCCTGTGAGATGTGCAAGTATGGACACTGTGTTT	TGCAACCCAGGCTTTGTGTGGCC	1998
Db	1804	CAGAGCCCTGTGAGATGTGCAAGTATGGCACTGTGTTT	TGCAACCCAGGATTTGTGTGGCC	1863
QY	1999	TCACATGTGACATACGCGCACTGACACAGCTCTCAGCT	TGTATTAATCAATGAAGGCTC	2058
Db	1864	CCAATGTGACATATGAGCAATT---CAGCTGTCAAGCT	TGCTATATATCAAGTGAAGATTTC	19220
QY	2059	AGATGATCAGTTTATGACGAGCTCCAGATCTGTGAGAG	CCCCCTGATTTTGAAGGCTCAGG	2118
Db	1921	AGATGATCAGTTTATGACGAGCTTTCAGAAATGAGAGG	CCCCCTGATTTTGAAGGCTCAGG	1980

QY	2119	G-----TGAGCAGCTACCCAGCCAGAGCTGGAGAGCAGAGTCCAGCAGGCTGAGCAGG	2172
Db	1981	GTGGTGATGAGTAGTAGTACTGATACAGAGCTGGAGAGGACAGGATGCACAGCAGCTGAGCAGG	2040
QY	2173	CCCTTCGGGACATCTCTGAGAGAACCCAGATTCCAGAAAGTGCCTTAAAGATCCCTCAATC	2232
QY	2233	TCCGGGTTGGCCAAAGCAGACCTCAAGAGATACCTACCGGAGCCGCTGGATGACCTCA	2292
Db	2101	TCAGATTGCCAAGGTGAGAGGCCAAGAGAACACTACAGAGCCGCTGGATGACCTCA	2160
QY	2293	AGATGACTGTGGAAAGAGTTCCGGCCCTTGGGCACTCAGTATCAGAACCAAGTTTCAGGATA	2352
Db	2181	AGATGACTGTGGAAAGAGTTCCGGCCCTTGGGCAAGTCAAGTACCAAGCCGAGTTGGGATA	2220
QY	2353	CTCCGAGGCTATCACTCAAGTGGCCCTGAGACCTGGAGAGAAAGTGAAGCTTCCCTGCMAA	2412
Db	2221	CTCAGAGCTCATACTCAGATGAGCTGAGACCTGGGAGAAAGTGAAGCTTCTTTGGGAA	2280
QY	2413	ACACCAATTCCTCTCTCAGAGCACTACGCGGGGCCAAATAGGCTTTAAAAAGTTGGCTC	2472
Db	2281	ACACTTAACATTCCTGCTCAGACCACTACGCGGGGCCAAATAGGCTTTAAAAAGTTGGCTC	2340
QY	2473	AGAGGCGCACAGATTGGCAGACAGCCATGTTCACTCAGCCAGCCAGTAACTGAGCAACTGG	2532
Db	2341	AGAGGCGCACAGATTAGCAGAAAGCCAGCTTGAGTCAAGCCAGTAACTGAGCAACTGA	2400
QY	2533	CAAAAGAAACCCAGAGATATTCCAAAGAGCTGATGTCACTGTGTCGCGAGGCTTCCAGG	2592
Db	2401	CAAGGAAACCTGAGAGCACTATTCCAAACAGCCCTCTCACTGCTGCGAGGCCCTGCTATG	2460
QY	2593	AAGGAG-----GGGGAAGGGGCGCCGCGGAGGAGCGCGTGTGTCAAAGGCTTTGGGAA	2646
Db	2461	AAGGAGTCCGGAAGCGGAGGCGGTAGCCCGGAGGCTGCTGTGTGTCAAAGGCTTTGGGAA	2520
QY	2647	AATTGCAGAAAACCTAAATCTCTGGCCCAAGAGTTGTGAGGGAGGCCACGCAAAACGACA	2706
Db	2521	AATTGCAGAAAACCAAGTCCCTGGGCCAGGAGTTGACAAAGGAGAGGCCACTCAACGGGAA	2580
QY	2707	TGGAAGCAGATAGGCTTATACAGCATAGTCTCCACCTTCTCAATTCGCTCTCAATTC	2766
Db	2581	TTGAAGCAGATAGGCTTATACAGCATAGTCTCCGCTCTCTGATTCAGTGTCTCTCGCTTC	2640
QY	2767	AGGAGTCATATGATCAGTCTTGGAGG --- AGAAGGGAAGAGGCTCAGACAAAACCTG	2823
Db	2641	AGGAGTCATATGATCAGTCTTGGAGG --- AGAAGGGAAGAGGCTCAGACAAAACCTG	2700
QY	2824	ATTCTCTCTCAAAACGTTGTGATCAAGCATATGAGATGAGTTCAAGCAGCTGCAAAAGCATC	2883
Db	2701	ATTCTCTCTCAAAACGTTGTGATCAAGCATATGAGATGAGTTCAAGCAGCTGCAAAAGCATC	2760
QY	2884	TGGGAACCTGGGAAGAGAAACCCGGCAGCTCTTACAGATGAGAAAGATGGAGACACA	2943
Db	2761	TGGGAACCTGGGAAGAGAAACCAACAGCAGCTCTTACAGATGAGAAAGATGGAGAGAGA	2820
QY	2944	CATCAGATCAGCTGCTTCCGCTGCCAACCTGCTTAAAGAGAGGCCAAGAACACATTA	3003
Db	2821	AATCAGATCAGCTGCTTCCGCTGCCAACTGCTTAAAGAGAGGCCAAGAACACACTGA	2880
QY	3004	GTATGGCAATAGCACTTTTATGAAAGTTGGAACATCTTAAACAAATCTCAGAGAGTTTG	3063
Db	2881	GTATGGCAATAGCCACTTTTATGAAAGTTGGAACATCTTAAACAAATCTCAGAGAGTTTG	2940
QY	3064	ACCTGCAGTTGAGATTAAGAGCAGAAAGCTGGAAGGCCATGAAAGACTCTCTCA	3123
Db	2941	ACCTGCAGTTGAGACAGAAAGCAGAAAGCTGGAAGGCCATGAAAGACTCTCTCA	3000
QY	3124	TCAGCCAGAAAGTTGCAAGTCCAGTACAGACAGAAAGCAAGCAAGCAAGCAGCCCTGGGCA	3183
Db	3001	TCAGCCAGAAAGTTTCAAGTCCAGTACAGACAGAAAGCAAGCAAGCAAGCAGCCCTGGGCA	3060

QY 3184 GTCTGCTGCTCCGACGCCAGAGGCAAGATGACGCCAGAGGCCCTGGAGATCTCTG 3243
 Db 3061 GCGCTGCTGCTGCTGACACAGAGGCAAGATGAGGGCCGCGGAGGCCCTGGAGATCTCTG 3120
 QY 3244 GCAAGATAGAAAGAGATGAGATGCTGAACTTGGAAAGCAATGTGACAGCATGAGAG 3303
 Db 3121 GTGAGATGAAAGAGATGAGATGCTGAACTTGGAAAGCAATGTGACAGCATGAGAG 3180
 QY 3304 CCTTGGCCATGAGAAAGGAGCTGCGCACTCTGAAAATGAGATGAGAAAGAGAG 3363
 Db 3181 CCTTGGCCATGAGAAAGGAGCTGCGCTCTCTGAAAGATGAGATGAGAAAGAGAG 3240
 QY 3364 AGCTGTCAAGAGAGAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 3423
 Db 3241 AGCTGTCAAGAGAGAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 3300
 QY 3424 CAGAGGCCCAAGAGATGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3483
 Db 3301 CAGAGGCCCAAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 3360
 QY 3484 TCAACACATTTGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 3543
 Db 3361 TCAACACATTTGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 3420
 QY 3544 GCGTGTCTTCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3603
 Db 3421 GCGTGTCTTCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3480
 QY 3604 GCGCTTGTATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3663
 Db 3481 GCGCTTGTATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3540
 QY 3664 TGGAGACTAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 3723
 Db 3541 TGGAGACTAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 3600
 QY 3724 AGCTGCCCCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3783
 Db 3601 AGCTGCCCCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3660
 QY 3784 ATTTCCTCAACCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3837
 Db 3661 ATTTCCTCAACCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3714

RESULT 5
 ABL49085
 ID ABL49085 standard; cDNA: 5156 BP.
 XX
 AC ABL49085;
 XX
 DT 01-MAY-2002 (first entry)
 XX
 DE Human lung tumour cDNA sequence for contig 20 SEQ ID NO:130.
 XX
 KW Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
 XX
 OS Immune response; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200200174-A2.
 XX
 PD 03-JAN-2002.
 XX
 PF 28-JUN-2001; 2001MO-US21065.
 XX
 PR 28-JUN-2000; 2000US-0606421.
 PR 02-AUG-2000; 2000US-0630940.
 PR 21-AUG-2000; 2000US-0643597.
 PR 15-SEP-2000; 2000US-0662786.
 PR 09-OCT-2000; 2000US-0685696.
 PR 12-DEC-2000; 2000US-0735705.
 PR 07-MAY-2001; 2001US-0850716.

XX (CORI-) CORIXA CORP.
 PA Wang T, Mang A, Skelky YAW, Li SX, Kaios MD, Henderson RA;
 PI McNeill PD, Fanger N, Reiter MM, Marnettaks M, Fanger GR;
 PI Vedvick TS, Carter D, Watanabe Y, Peckham DW;
 XX WPI: 2002-090513/12.
 XX
 PT Polynucleotides encoding lung tumor polypeptides, useful for treating
 XX lung cancer or stimulating an immune response -
 PS Example 3; Page 236-237; 374pp; English.
 XX
 CC The present invention describes human lung tumor proteins. Human lung
 CC tumor proteins and polynucleotides have cytostatic and immunostimulant
 CC activities, and can be used in vaccine production. Compositions
 CC comprising the lung tumor proteins, polynucleotides, antibodies,
 CC fusion proteins, T cell populations, or antigen presenting cells that
 CC express the lung tumor proteins are useful for treating lung cancer or
 CC stimulating an immune response. ABL48959 to ABL49300 and ABL74946 to
 CC ABL75070 represent sequences used in the exemplification of the present
 CC invention.
 XX
 SQ Sequence 5156 BP; 1351 A; 1222 C; 1377 G; 1206 T; 0 other;
 Query Match 74.1%; Score 2956.4; DB 24; Length 5156;
 Best Local Similarity 88.4%; Pred. No. 0;
 Matches 3285; Conservative 0; Mismatches 401; Indels 28; Gaps 6;
 QY 146 CAGAGGCGCGGAG 198
 Db 7 CAGAGGCGCGGAG 66
 QY 199 TGCCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 258
 Db 67 TGCCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 126
 QY 259 CCACCTCCGGGAGGAGAGTCTGTGATGCAACGGAAGTCCAGCAATGATCTTGAAC 318
 Db 127 CCACCTCCGGGAGGAGAGTCTGTGATGCAATGGAAGTCCAGCAATGATCTTGAAC 186
 QY 319 AGCACTTCAACAAG 378
 Db 187 AGCACTTCAACAAG 246
 QY 379 ATGCACTTCAAG 438
 Db 247 ATGCACTTCAAG 306
 QY 439 GTTACCTGCAATGTAATCTTAAAGGTTCTTAAAGGTTCTTAAAGGTTCTTAAAGGTT 498
 Db 307 GTTACCTGCAATGTAATCTTAAAGGTTCTTAAAGGTTCTTAAAGGTTCTTAAAGGTT 366
 QY 499 GGTGACGCTGTAAG 558
 Db 367 GGTGACGCTGTAAG 426
 QY 559 ACACACTCTGATGATGCTGGTGGCCAGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 618
 Db 427 ACATGCTCAAG 486
 QY 619 GTGACCCAGCTGATCTCAGAGGCGCTGTGACTCAGAGGCGCTGTGCTGCTCAGAGGCG 678
 Db 487 GTGACCCAGCTGATCTCAGAGGCGCTGTGACTCAGAGGCGCTGTGCTGCTCAGAGGCG 546
 QY 679 TCACCTGAGAGAGGCTGTGATGCTGCAACAGAGTACTATCACTGATGAGAGAGAGAG 738
 Db 547 TCACCTGAGAGAGGCTGTGATGCTGCAACAGAGTACTATCACTGATGAGAGAGAGAG 606
 QY 739 CTCAGGCGCTGATCCAGAGTCTTGTGCTTAAAGGAGATCCAGAGCTCCAGAGCTCGGG 798
 Db 607 CTCAGGCGCTGATCCAGAGTCTTGTGCTTAAAGGAGATCCAGAGCTCCAGAGCTCGAG 666

OY	799	ACTGACGTGTCATAAATAATCATCTCTGCTTCCATCAAGATGTTGATGCTGGAGGCTG	858
Db	667	AATACAGATGTCATAAAGATACCTCTACCTTCTCAAGATGTTGATGGCTGGAGGCTG	726
OY	859	TCCAAAGAAAGGGGTCCTGCAAAAGGTCACAGTGGTCACAGGGGCATCGGATATATTTA	918
Db	727	TCCACAGAAATGGGTCTCTGCAAAAGCTCCATGTTGATACAGCCCATCAAGATGTGTTA	786
OY	919	GCTCAGCAGCAGATCAGACCTGTCATATTTGTAGTCTGCCAAATTTCTTGGGATC	978
Db	787	GCTCAGCCCAAGCAGACTAGACCTGTCTATTTTGTGGCTCGCCAAATTTCTTGGATC	846
OY	979	AACAGGTGAGCTACGGGCAAAAGCTATCTTTTGTACTACCGTGGATAGGGGAGCGAC	1038
Db	847	AACGGTGAAGTATGTCGTAAGGCTGTCCTTTGACTACCGTGGTGAACAGAGGAGCGAC	906
OY	1039	ACCATATCGCCATGACGTGATCTCTGGAAGTGCCTGGTCTACGAGTACAGCTCCCTGTA	1098
Db	907	ACCATCTGCCCATGATGTGATTTCTGGAAGTGTGTGATCTACAGGATCAGAGCTCCCTGA	966
OY	1099	TGCCACTTTAGCAAGACACTGCTTTGTGGATCACCAGACTTACATTCAGATTAATG	1158
Db	967	TGCCACTTGGCAACACTGCTTTGTGGCTCACCAAGACTTACACATTCAGGTTAATG	1026
OY	1159	AACATCCAGAGATTAATTTGGAGCCCGCAGCTAACTTACTTTGACTATCGGAGGTTACGC	1218
Db	1027	AGCATCCAGCAATTAATTTGAGGCCCCCAAGCTGAGATTACTTGAATATCGAAGTTACTCC	1086
OY	1219	GGAACCTCACAGCCCTGCGATCCGAGCTACCTACGGAAGATACAGTACTGGTACATYG	1278
Db	1087	GGATCTCACAGCCCTCGCATCCGAGCTACATATGAGAATATACGTAAGTGGTAACTYG	1146
OY	1279	ACAACGTGACCTTATTTACGCCCGCCCGCTTTCTGAGAGCCCGCCCTGGGTTGAC	1338
Db	1147	ACAATGTACCTTATTTACGCCCGCCCTGTCTGTGAGGCCCAAGCACCCCTGGGTTAAC	1206
OY	1339	AATGTGATGCGCTGTGGCTGACACAGGGGCGAGTCTGCACAGATTGTGCTCCGCTACA	1398
Db	1207	AGTGTATATGTCGTTGGGTACAAAGGGCAATTCTGCAGAGATTGTGCTCTGTGGTACA	1266
OY	1399	AAAGAGATTCAGCCAGACTGGGACCTTTTGGCACCTGTATTCATGTATCTCCAGAGGG	1458
Db	1267	AGAAGATTCAGCCAGACTGGGCGCTTTTGGCACCTGTATTCCTGTAACTGTCAAGGGG	1326
OY	1459	GAGGGCGCTGGATTCAGACAGACAGAGAGCTTTACTCAGGGGATGAGAACCTCTACATTC	1518
Db	1327	GAGGGCGCTGTGATTCAGACACAGAGAGATTTTATTCAGGGGATGAGATCTCAAT--	1384
OY	1519	CTGAGTGTCTGACTGCCCATCTGTTGTTCTACAAGATCCACAAGACCCCGCAGCTGCA	1578
Db	1385	-TGAGTGTGCTGACTGCCCATTTGTTGTTCTACAAGATTCAGACAGCCCGCAGCTGCA	1443
OY	1579	AGCGTGGCCCTGTGTCGAATGGGTTTCAGTCTCTCGATGATCCGAGACAGAGAGGTGG	1638
Db	1444	AGCCATGTCTCTGTATACGGGTTCAGCTCTCATGTATCCCGAGACGGAGAGAGGTGG	1503
OY	1639	TGTCAATATACGTGCCCCAGGGGTCTACATGTGTGCCCGGTGTGAGCTCTGTCTATGGCT	1698
Db	1504	TGTCAATATACGTGCCCTCCGGGGTACACGGTGTGCCCGGTGTGAGCTCTGTCTATGGCT	1563
OY	1699	ATTTTGGGGACCCCTTCCGGGACAGTGGCCCAAGTGAAGGCTTTGTACGCTCTGTACGTCA	1758
Db	1564	ACTTTGGGGACCCCTTGTGTGAACATGGCCCAAGTGAAGGCTTTGTACGCTCTGTACGTCA	1633
OY	1759	ACAACAACGTGGACCTTGTGCTCTCCGGGAAGTGTGACCGGCTGACAGGCAAGGTGTGGA	1818
Db	1624	ACAACAATGTGGACCCCAAGTGTCTCTGGGAATTGTGACCGGCTGACAGGCAAGGTGTTGA	1683
OY	1819	AGTGCATCCACAACAGCTGGGGTCCACTGTGACCAAGTGTGAAAAGCAGGCTACTATGCGG	1878
Db	1684	AGTGTATCCACAACAGCGGGATCTCTCTCGACCAAGTGTGAAAAGCAGGCTACTATGCGG	1743

QY	1879	ACCCTTGCGCTCCCAATCCAGACACAAGTGTGAGCTTGTGCACTGCAACCCAGTGGCT	1938
Db	1744	ACCCATTGTGGCTCCCAACCCAGACACAAGTGTGAGCTTGTGCACTGCAACCCAGTGGCT	1803
QY	1939	CGAGAGCCGTGTGAGTGTGCAAGTATGTGGCAGCTGTGTTTGCAGAGCCAGGCGTTGTGTGCC	1998
Db	1804	CAGAGCCTGTAGAGTGTGCAAGTATGTGGCAGCTGTGTTTGCAGAGCCAGGATTTGTGTGCC	1863
QY	1999	TCAGCTGTGACGATCGCGCACGTGCAAGCTGTCCAGCTTGTCTAATCAAGTGAAGTTTC	2058
Db	1864	CCAACGTGACATGAGAGCAATT---CAGCTGTCCAGCTTGTCTAATCAAGTGAAGTTTC	1920
QY	2059	AGATGATCACTAATTATCAGACGCTCCAGATCCTGGAGGCCGTGATTTGCAGAGCTCAGG	2118
Db	1921	AGATGATCACTAATTATCAGACGCTCCAGATCCTGGAGGCCGTGATTTGCAGAGCTCAGG	1980
QY	2119	G-----TGAGACAGTACCCAAACCAGAGCTGGAAGGAGCAGATGACAGACGCTGAGCAGG	2172
Db	1981	GTGGTGAATGAGTAGTGTACCTGTATACAGAGCTGGAAGGAGCAGATGACAGACGCTGAGCAGG	2040
QY	2173	CCCTTCGGGACATTTCTGAGAGACCCAGATTTTCAAGAATGCTGTAGATCCTTCAATC	2232
Db	2041	CCCTTCAGAGCAATTTCTGAGAGATCCCAAGATTTTCAAGAAGGCTGAGCAGATCCTTGTGTC	2100
QY	2233	TCGGAGTGGCCAAAGCAAGCACTCAAGAAATAGCTACCGGAGACCGCTGATGACCTCA	2292
Db	2101	TCAGATGTGGCCAAAGTGAAGGCCAAGAAGAACACTACAGAGCCGCTGTGATGACCTCA	2160
QY	2293	AGATGACTGTGAAAAGAGTTGCGGCCCTTGGGACGTCAGTATCAGAACCAAGTTCAAGATA	2352
Db	2161	AGATGACTGTGAAAAGAGTTGCGGCCCTTGGGACGTCAGTATCAGAACCAAGTTTGGGATA	2220
QY	2353	CTCGAGGCGCTATACACAGTATGGCGCTGAGCCGTGGAGAAAGTGAAGCTTCCCTGCATA	2412
Db	2221	CTCGAGGCGCTATACACAGTATGGCGCTGAGCCGTGGAGAAAGTGAAGCTTCCCTTGGGATA	2280
QY	2413	ACACCAATTTCTCTTCACAGAGCACTACGTGGGGGCCAAATGCGTTTAAAAAGTTGTGCTC	2472
Db	2281	ACACTAACTTCTGCGCTCAGAACCACTACGTGGGGGCCAAATGCGTTTAAAAAGTTGTGCTC	2340
QY	2473	AGGAGGCCACAGATTTGGCAGACAGCCATGTTCAAGTACAGCAGTAACTGAGACACTGG	2532
Db	2341	AGGAGGCCACAGATTTAGCAGAAAAGCCACGTGTGAGTACGCCAGTAACTGAGACACTGA	2400
QY	2533	CAAGAGAAACCCAGAGATATTCCAAAGAGCTGATGTACTGTCTCGGAGGCTCTGCAGG	2592
Db	2401	CAAGGAAACTGAGAGCACTATTCCAAACAAGCCCTCTCACTGTGTGCGCAAGGCCCTTGATG	2460
QY	2593	AAGGAG-----GCGGAAAGCGGACGCTGACGAGCCGTGTGCAAAAGCTTGTGGAA	2646
Db	2461	AAGGAGTGTGAAAGCGGAAAGCGGTAGCCCGGAGCGGTGTGTGTGCTCAAGAGGCTTGTGGAA	2520
QY	2647	AATTGCAAAAATTAATCTCTGGGCCAGAGTTGTGAGAGGAGGCCACGCAACCCACA	2706
Db	2521	AATTGCAAAAATTAATCTCTGGGCCAGAGTTGTGAGAGGAGGCCACCTCAAGCGGAAA	2580
QY	2707	TGGAAGCAGATAGTCTTATCAGCATAGTCTCCACCTTCTCAATTCCTGTCTCAGATTC	2766
Db	2581	TTGAAGCAGATAGTCTTATCAGCATAGTCTCCACCTTCTCAATTCAGTGTCTGTGCTTC	2640
QY	2767	AGGAGTCAATAGATCAGTCTTTCGACGG---AGAAAGGAGAGGCTCAGCAAAAACCTG	2823
Db	2641	AGGAGTCAATAGATCAGTCTTTCGACGGGGAAGGAGCAAAAAGGATCAACAAAAAGGCG	27000
QY	2824	ATTCTCTCTCAAAACCGTGTGACTAAGCATATGATGATGATTCAAACAGCTGCAAAAGCATC	2883
Db	2701	ATTCTCTCTCAAGCGCTGTATACAGGCATATGATGATGATTCAAACAGTAAAGATC	2760
QY	2884	TGGGAACCTGGGAAGAGAAAACCCGGCAGCTCTTACAGATATGAAAGAAATGTGGAGACAGA	2943
Db	2761	TGGGAACCTGGGAAGAGAAAACAGCAAGCTCTTACAGAAATGTGGAGAGAGA	2820
QY	2944	CATCAGATCAGCTGCTTCCGTGCAAACTTGTCTAAAGAGCAGAGCCCAAGACACTAA	3003

Db 448 CAACTGACGTGACACCGACGTCGACGAGGCGCCGTGACGCGGCGCGCTGTGCTG 507
Qy 668 CAACCGCGCTGTCAGTCGAGAGCGCTGTGATAGGTGTCGACGAGTTACTATCAGCTGGA 727
Db 508 CAACCCAGCTGTACTGAGAGACGCTGTGATGGGTGTGATGACAGTTACTAATATCTGGA 567
Qy 728 TGGGGGAAACCCCTCAGGCGCTGTACCAAGTGTGTTGCTATGGGATTCCGCGACAGTCCA 787
Db 568 TGGGGGGAACCCCTCAGGCGCTGTACCAAGTGTGTTGCTATGGGATTCCGCGACAGTCCA 627
Qy 788 CAGCTCTGGGAGCTACAGTGTCCATAAATCATCTGTGCTTCCATCAAGATGTTGATGG 847
Db 628 CAGCTCTGCAAGAAATACAGTGTCCATAAATCATCTGTGCTTCCATCAAGATGTTGATGG 687
Qy 848 CTGGAAGGCTGTCCAAAGAAACGGGTCTCCGCAAACTCCAGAGTGTACAGGCCCATCG 907
Db 688 CTGGAAGGCTGTCCAAAGAAATGAGGTCTCCGCAAACTCCAGAGTGTACAGGCCCATCA 747
Qy 908 GGATATATTTAGCTCAGCAGACGATCAGACCTGTCTATTTTGTAGCTCCGCAAAAT 967
Db 748 AGATGTGTTAGCTCAGCAGACGATCAGACCTGTCTATTTTGTAGCTCCGCAAAAT 807
Qy 968 TCTTGGGAATCAGAGTGAAGTACGGGCAAAAGCCTATCTTTGACTAAGCTGTGATAG 1027
Db 808 TCTTGGGAATCAGAGTGAAGTACGGGCAAAAGCCTGTCTTGTACTAAGCTGTGATAG 867
Qy 1028 GGGGAGGAGACACCATCTGCCCCAGTACGTCGATCTCCGGAAGTCTGTCTACGAGATCAG 1087
Db 868 AGGAGGAGACACCATCTGCCCCAGTACGTCGATCTCCGGAAGTCTGTCTACGAGATCAG 927
Qy 1088 AGCTCCCTGTGATGCTAGCTAGCAGACACTGCTTGTGGATCAGCAAGACTTACACTT 1147
Db 928 AGCTCCCTGTGATGCTAGCTAGCAGACACTGCTTGTGGATCAGCAAGACTTACACTT 987
Qy 1148 CAGATTAAATGACATCCAAAGCAGATAATGGAGCCCCAGCTAAATCTTTGATATCG 1207
Db 988 CAGATTAAATGACATCCAAAGCAGATAATGGAGCCCCAGCTAAATCTTTGATATCG 1047
Qy 1208 GAGGTACTGCGGAACTCAGACGCTGCGGATCCGAGCTACCTACGAGAAATACAGTAC 1267
Db 1048 AAGGTACTGCGGAAATCAGACGCTGCGGATCCGAGCTACCTACGAGAAATACAGTAC 1107
Qy 1268 TGGGTACATGACAACTGACCTGATTTAGCCCGCCGCTTCTGGAGCCCCAGCGCC 1327
Db 1108 TGGGTACATGACAACTGACCTGATTTAGCCCGCCGCTTCTGGAGCCCCAGCGCC 1167
Qy 1328 CTGGGTGAAACATGATGATGCTGTTGGCTACAGAGGCGAGTTCTGCGAGATTTGCG 1387
Db 1168 CTGGGTGAAACATGATGATGCTGTTGGCTACAGAGGCGAGTTCTGCGAGATTTGCG 1227
Qy 1388 TTCCGGGTACAAAGAGATTCAGGCACTGGGACCTTTGGCACTGATTCATCATGTA 1447
Db 1228 TTCTGGGTACAAAGAGATTCAGGCACTGGGACCTTTGGCACTGATTCATCATGTA 1287
Qy 1448 CTGCAAGGAGGAGGCGCTGCGATCCAGACAGAGAGCTGTACTCAGGAGATGAGAA 1507
Db 1288 CTGCAAGGAGGAGGCGCTGCGATCCAGACAGAGAGATGTATTTCAGGAGATGAGAA 1347
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Qy 1568 CCGGAGTGCAGAGCGCGTCCCTGTCCGCAATGGGTTACGCTGCTCCGATGCTGAGAC 1627
Db 1405 CCGGAGTGCAGAGCGCGTCCCTGTCCGCAATGGGTTACGCTGCTCCGATGCTGAGAC 1464
Qy 1628 AGAGAGGTGTGTGCAATTAAGTCCCAAGGAGTGTCACTGAGTCCGCTGTGAGCTGTG 1687
Db 1465 GGAAGAGGTGTGTGCAATTAAGTCCCAAGGAGTGTCACTGAGTCCGCTGTGAGCTGTG 1524
Qy 1688 TGTGTAGTGTATTTTGGGAGACCCCTTGGGGGAAAGTGGCCAGTGAAGCCCTTTCAGCC 1747
|||||

Db 1525 TGTGTAGTGTACTTTGGGAGACCCCTTGTGTGAACATGAGCCAGATGAGGCGCTTGCAGCC 1584
Qy 1748 CTGTGAGTGCAGAACAAACAGTGAACCTAGTCCCTCCGAGAACTGTGACCCCTGACAGG 1807
Db 1585 CTGTGAATGCAACAAACAGTGAACCTAGTCCCTCCGAGAACTGTGACCCCTGACAGG 1644
Qy 1808 CAGGTGTCTGAAGTGCATCCACAAACAGTGGGGGTGCACATGTGACGAGTCAAGAGCAG 1867
Db 1645 CAGGTGTCTGAAGTGCATCCACAAACAGTGGGGGTGCACATGTGACGAGTCAAGAGCAG 1704
Qy 1868 CTACTATGAGGAGACCCGTTGCTCCCATTCAGACAGACAGTGTGAGGCTTGCACATGCA 1927
Db 1705 CTACTATGAGGAGACCCGTTGCTCCCATTCAGACAGACAGTGTGAGGCTTGCACATGCA 1764
Qy 1928 CCCAGTGGGCTCCGAGGCTGTGAGTGTCCAAAGTATGAGGAGTGTGTTTCCAGCCAGG 1987
Db 1765 CCCAGTGGGCTCCGAGGCTGTGAGTGTCCAAAGTATGAGGAGTGTGTTTCCAGCCAGG 1824
Qy 1988 CTTTGTGGGCTCAGCTGTGAGTGTGCGGACCTGACACAGTGTCCAGCTTGTATATCA 2047
Db 1825 ATTTGTGGGCTCCCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1881
Qy 2048 AGTGAAGTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2107
Db 1882 AGTGAAGTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1941
Qy 2108 GAAAGCTCAGG-----TGAGCAGTATCCCAAGCAGAGTGTGAAGGACAGATGACCA 2161
Db 1942 AAAGGCTCAGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2001
Qy 2162 GCGTGAAGAGGCGCTTGGGACATTTGTGAGAAAGCCAGATTTACAAAGATGCTGATTT 2221
Db 2002 GCGTGAAGAGGCGCTTGGGACATTTGTGAGAAAGCCAGATTTACAAAGATGCTGATTT 2162
Qy 2222 ATCTTCAATCTCCGGGTGCGCAAGGAGCTCAAGAGATTAAGTACCGGAGCCGCT 2281
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Qy 2282 GGATGACCTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2341
Db 2122 GGATGACCTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2181
Qy 2342 AGTTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2401
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Qy 2402 TTCCCTGCAAAACCAACATTTCTCTTCAAGACCTACGCTGGGCGCAATGCTTTAA 2461
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Qy 2462 AAGTGTGGCTCAGAGGCGCAGATGAGTGGCAGACAGCCATGTCAGTACAGCAGTACAT 2521
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Qy 2522 GGAGCACTGCAAAAGGAAACCCAGAGTATTCGAAAGAGTGTGATGATGATGATGATGATG 2581
Db 2362 GGAGCACTGCAAAAGGAAACCCAGAGTATTCGAAAGAGTGTGATGATGATGATGATGATG 2421
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Qy 2636 GCTTGTGGGAAATTTGCAAGAACTAATCTCTGCGCCAGAGATTTGTGAGGAGGCGCAG 2695
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Db 2542 TCAAGCGGAATTTGAAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATG 2601
Qy 2756 GTCTCAGATTCAGGAGTCAATGATCAGTCTTCCAGT---AGAAGGAGAGGCTCAG 2812
Db 2602 GTCTCAGTTCAGGAGTCAATGATCAGTCTTCCAGT---AGAAGGAGAGGCTCAG 2661
|||||

Db 2457 AAGAGTCGAGAGCGGAGCGGTAACCCGAGCGTCTGTGTGTCAGAAAGGCGTTGTGAAA 2516
QY 2647 AATTGAGAAAATAAATCTCTGCGCCAGAGTGTGTGAGGAGGCGCCAGCAACCGACA 2706
Db 2517 AATTGAGAAAACCAAGTCCCTGGCCAGCAGTGTGACAAAGGAGGCGCAGCTCAAGCGGAAA 2576
QY 2707 TGGAGAGATAGTCTTATCAGCATATGTCTCCACCTTCTCAATTCCTGTCTCAGATTTC 2766
Db 2577 TTGAGAGATAGTCTTATCAGCATATGTCTCCGCGCTCCGAGATTCAGTGTCTCGGCTTC 2636
QY 2767 AGGAGATCAATGATCAGTCTCTTGAGGT--AGAGGAGAGAGGCTCAGACAAAAGCTG 2823
Db 2637 AGGAGATCAATGATCAGTCTCTTGAGGTGAGAGAGAGAGAGATCAACAAAAGCGG 2696
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QY 3064 ACCTGCAAGTGTGAGATTAAGAGAGCAAGCTCAAGAGGCGATGAGAGACTCTCTCA 3123
Db 2937 ACCTGCAAGTGTGAGATTAAGAGAGCAAGCTCAAGAGGCGATGAGAGACTCTCTCA 2996
QY 3124 TCAGCCAGAGATGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 3183
Db 2997 TCAGCCAGAGATGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 3056
QY 3184 GTCTGCTGCTGCGAGCGCCAGAGGCGAAAGATGACAGGAGGCGCCCTGAGATCTCTG 3243
Db 3057 GCGCTGCTGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 3116
QY 3244 GCAAGATAGAGAGAGAGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 3303
Db 3117 GTGAGATAGAGAGAGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 3176
QY 3304 CCTTGGCCATGAGAGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 3363
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QY 3604 GCGCCCTTGTATGTGAGAGTGTGAG 3663
Db 3477 GCGCCCTTGTATGTGAGAGTGTGAG 3536
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Db 3597 ACCTGCCCCCGGCTGTCTACAAATACCAGGCTCTTGAGCAACAGTGAAGCTGTAGAG 3656
QY 3784 ATTCTCTCAACCAAGTCTTGGATTCAGACCTAGCTGCTTGAAGATTCTCA 3837
Db 3657 ATTCTCTCAACCAAGTCTTGGATTCAGACCTAGCTGCTGAGGCTGAGGAGCATGTCA 3710
RESULT 8
ID AAD31145 standard; cDNA; 3582 BP.
XX AAD31145;
AC AAD31145;
XX 21-AUG-2002 (first entry)
DT 21-AUG-2002 (first entry)
XX Human laminin gamma2 chain cDNA.
DE Human laminin gamma2 chain cDNA.
XX Cancer; cell proliferation; integrin receptor; signalling pathway;
KW gene therapy; human; laminin gamma2; ss.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT CDS 1..3582
FT /tag= a
FT /product= "Laminin gamma2 chain"
XX
XX W0200230465-A2.
XX
XX 18-APR-2002.
XX
XX 12-OCT-2001; 2001MO-US32127.
XX
XX 12-OCT-2000; 2000US-239705P.
XX 24-OCT-2000; 2000US-242812P.
XX
XX (UNIV ROCHESTER.
XX
XX Land H, Deleu L;
XX WPI; 2002-416838/44.
XX P-PSDB; AAE14712.
XX
XX Reducing proliferation of cancer cell, by inhibiting ligand binding to
PT integrin receptor on cell, reducing integrin-integrin interaction,
PT receptor clustering interaction or integrin-non-integrin protein
PT interaction -
XX
XX Disclosure; Page 85-86; 148pp; English.
XX
XX The invention relates to a method of reducing proliferation of cancer
XX cells, comprising inhibiting ligand binding to integrin receptor on
XX cancer cells, where integrin receptor comprises integrin, reducing
XX integrin-integrin interaction, integrin receptor clustering interaction
XX or integrin-non-integrin protein interaction, reducing production of
XX integrin or ligand of integrin receptor by cancer cells, or
XX interfering with integrin-signalling pathway. The present sequence
XX is human laminin gamma2 chain cDNA.
XX
XX Sequence 3582 BP; 938 A; 872 C; 1026 G; 746 T; 0 other;
SQ
Query Match 72.8%; Score 2904; DB 24; Length 3582;
Best Local Similarity 89.1%; Pred. No. 0;
Matches 3197; Conservative 0; Mismatches 370; Indels 21; Gaps 5;
QY 198 ATGCTGCGCTGTGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 257
Db 1 ATGCTGCGCTGTGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 60
QY 258 GCCACCTCCGGAGGAGAGTGTGTGTGTGATTCACACGGAATCTCAGGCAATGCAATCTTTGAC 317

Db 61 GCCACCTCCAGAGAGGAGTCTGTGATTCGAATGGGAAGTCCAGGACAGTGTATCTTGAT 120
Oy 318 CAGGAACTTCACAAACAGACAGAAATGGATTCGCGTCCCACTGCAATGCACAAACCT 377
Db 121 CGGAACTTCACACAAACAGTGTAAATGGATTCGCGTCCCACTGCAATGCACAAACCT 180
Oy 378 GATGGCACTCACCTCGAGAGGTGCAAGGACAGATTTTACGACAGAGAAAGGAGCCG 437
Db 181 GATGGCACTCACCTCGAGAGGTGCAAGATGGCTTTTACGCGCACAGAGAAAGGAGCCG 240
Oy 438 TGTTTACCTTCGAAATGTACTGTAAAGTTCCTTTAGCGCTCGATGTGACACTCTGGA 497
Db 241 TGTTTGCCCTTCGAATTTGAATCCAAAGTTCTCTTAAGTCTCGATGTGACACTCTGGA 300
Oy 498 CGGTCGAGCTGTAGCCAGGTGTGACAGAGACAGGTGTGACCATGTCTCCCGGCTTC 557
Db 301 CGGTGACAGCTGTAAACAGGTGTGACAGAGACCCAGATGTCTGCTCCAGGCTTC 360
Oy 558 CACACACTCACTGATGCTGGGTGGCCCAAGACCAAGGCTGTAGACTCCAAAGTGTAC 617
Db 361 CACATGCTCACAGATGGGGGTGCACCCAGACAGAGACTGTAGACTCCAAAGTGTAC 420
Oy 618 TGTGACCCAGCTGACATCTCAGGGCCCTGTGACTCAGGCGCTGTCTGTCGACAGCCGCT 677
Db 421 TGTGACCCAGCTGACATCTCAGGGCCCTGTGACGCGGCGCTGTCTGTCGACAGCCACT 480
Oy 678 GTCACTGGAGAGCCGTGTGATAGTGTGACAGGACAGTGTACTATCACTGTGATGGGGGAAC 737
Db 481 GTTACTGTGAGAACCTGTGATAGGTGTGATCAGGTTAACTTAACTGTGATGGGGGAAC 540
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Db 541 CCTGAGGCGTGTACCAGTGTGTTTGTATGGGATTCGCGCAGCTGCGCAGCTCTGCA 600
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Oy 858 GTCCAAAGAAAGGGTCTCCGCAAAAGCTGCAGTGTGACAGGCGCACCGGATATATTT 917
Db 661 GTCCAAAGAAATGGGTCTCCGCAAAAGCTGCATCAATGGTACAGCGCATCAAGATGTT 720
Oy 918 AGCTCAGCAGCAGATCAGACCTGTCTATTTTGTAGTCTCCCAATTTCTTGGGAAT 977
Db 721 AGCTCAGCAGCAGATCAGACCTGTCTATTTTGTAGTCTCCCAATTTCTTGGGAAT 780
Oy 978 CAACAGTGTAGCTACGGGCAAAAGCCTATCTTTGACTACCGTGTGATAGGGGAGCAGA 1037
Db 781 CAACAGTGTAGCTATGGGCAAAAGCCTCTTTGACTACCGTGTGACAGAGAGGACAGA 840
Oy 1038 CACCATCTGCGCATGTAGTATCTGGAAGTGTGCTGTACAGGATACAGCTCCCTG 1097
Db 841 CACCATCTGCGCATGTATGTGTGGAAGTGTGCTGTACAGGATACAGCTCCCTG 900
Oy 1098 ATGCCACTTACCAAGACACTGCTGTGTGGATCAACAGACTTACACTTATAGATTAAT 1157
Db 901 ATGCCACTTACCAAGACACTGCTGTGTGGATCAACAGACTTACACTTATAGATTAAT 960
Oy 1158 GAACATCCAAAGCAGTAAATTTGAGGCCCCAGCTAAAGTACTTGAATGTGAGATTACTG 1217
Db 961 GAGATCCCAACCAATTAATTTGAGGCCCCAGCTGATTAATTTGAATGTGAGATTACTG 1020
Oy 1218 CGGAACCTCACAGGCGCTGCGGATCGAGACTACAGGAGAATACAGTACAGTGGGACTT 1277
Db 1021 CGGAATCTCACAGGCGCTCCGATCGAGACTACATATGAGAAATACAGTACAGTGGGACTT 1080
Oy 1278 GACAACGTGACCTGTGATTTACGCCGCCCTTTCTGAGGCCAGCGCCCTGGGTTGA 1337
Db 1081 GACAATGTGACCTGTGATTTACGCCGCCCTTTCTGAGGCCAGCGCCCTGGGTTGA 1140
Oy 1338 CAATGTGATCCCTGTTGGCTACAAAGGCGAGTTCTGCGAGATTGTCTTCGGGCTAC 1397
Db 1141 CAATGTGATCCCTGTTGGCTACAAAGGCGCAATTTCTGCCAGATTGTCTTCGGGCTAC 1200
Oy 1398 AAAGAGTTTACAGCAGACTGGACCTTTTGGACACTGTATTCATGTAACTGCAAGG 1457
Db 1201 AAGAGATTTACAGGAGACTGGGCTTTTGGACACTGTATTTCTTTACTGTCAAGG 1260
Oy 1458 GGAGGGGCTTCGATCCAGACACAGAGACTGTACTCAGGGGATGAGAAACCTTGACATC 1517
Db 1261 GGAGGGGCTTCGATCCAGACACAGAGATGTTATTACAGGGATGAGAAATCTGACAT - 1319
Oy 1518 CCTAGTGTGCTGACTGCCCCATTGTTTCTACACAGATCCACAAGACCCCGCAGCTGC 1577
Db 1320 --TGAGTGTGCTGACTGCCCCAATTGTTTCTACAAACATCCGACAGACCCCGCAGCTGC 1377
Oy 1578 AAGCGTGGCCCTTCGCAATGGGTTGACGTGCTCCGAGATGGCTGACAGACAGAGAGTG 1637
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Oy 1638 GTGTCAATTAACCTGCCCCAGAGGTGTCACTGATCCGCGTGTGAGCTCTGTGTGATGGC 1697
Db 1438 GTGTCAATTAACCTGCCCCAGAGGTGTCAACCGGTGCGGCTGTGAGCTCTGTGTGATGGC 1497
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Db 1618 AAGTCAATCCAAACACAGCGCGCATCTACGTGACACAGTGCAAAGCAGGCTACTGTGGG 1677
Oy 1878 GAACCGTGGCTCCCAATCCAGCAGACAGATGTGAGCTTGCATCACTGCACCCAGTGGGC 1937
Db 1678 GAACCGTGGCTCCCAACCCAGCAGACAGATGTGAGCTTGCATCACTGCACCCAGTGGGC 1737
Oy 1938 TCGGAGCGCTGTGGAGTGTGGAAGTGTGAGGAGCTGTGTTTCAAGCCAGGCTTGTGGTGGC 1997
Db 1738 TCGAGCGCTGTAGAGTGTGGAAGTGTGAGGAGCTGTGTTTCAAGCCAGGAGTTTGTGGC 1797
Oy 1998 CTCAGCTGTGAGCATGTGCGCACTGACAGCCTGTCCAGCTTCTATTAATCAAGTAAAGTT 2057
Db 1798 CCCAAGTGTGAGCATGTGAGCAT--CAGCTGTCCAGTGTCTTAATCAAGTAAAGTT 1854
Oy 2058 CAGATGATCACTTATGACAGCAGCTCCAGATCCTGAGGCGCTGTATTCGAAGCTCAG 2117
Db 1855 CAGATGATCACTTATGACAGCAGCTCCAGATCCTGAGGCGCTGTATTCGAAGCTCAG 1914
Oy 2118 GG-----TGGAGCAGTACCCCAAGCAGAGCTGGAAAGCAGAGTGCAGCAGCTGAGCAG 2171
Db 1915 GGTGTGATGAGTATGTAATCTGTATACAGAGCTGGAAAGCAGAGTGCAGCAGCTGAGCAG 1974
Oy 2172 GCCCTTGGGCAATTTCTGAGAGAAAGCCAGATTTCAAGATGCTGTTAGATCCTTCAT 2231
Db 1975 GCCCTTGGGCAATTTCTGAGAGATGCCCCAGATTTCAAGAGTGTGAGCAGATCCTTGT 2034
Oy 2232 CTCGGGTTGGCCAAAGGACATCAGAGATAGCTACCGGAGCCGCTGTGATGACCTC 2291
Db 2035 CTCAGTGTGGCCAAAGGTGAGGACCAAGAGACAGCTACCGAAGCCGCTGTGATGACCTC 2094
Oy 2292 AAGATGACTGTGGAAGAGTTCGGGCGCTGGGAGTCAAGTATCAAGAACCAAGTTCAGAT 2351
Db 2095 AAGATGACTGTGGAAGAGTTCGGGCTGTGGAAAGTCAAGTACCGAAGCCGATGGGAT 2154
Oy 2352 ACTGCAAGCTCATCTCAGATGCGCTGAGCCTGGAAGAGTGAAGCTTCCCTGCA 2411
Db 2155 ACTGCAAGGCTCATCTCAGATGAGCTGAGCCTGGGAGAGAGTGAAGCTTCCCTGGA 2214
Oy 2412 AACACCAATTCCTCTTACAGACATCTAGTGGGCGCAATGCGCTTTAAAGTGTGGCT 2471
Db 2215 AACACTAACATTCCTCTTACAGACACTACGTGGGCGCAATGCGCTTTAAAGTGTGGCT 2274

Db 1141 CAGTGTATATGTCCTGTTGGGTACAAAGGGCAATTTCTGCCAGATTGTCTTCTGGCTAC 1200
Oy 1398 AAAGAGTTTACAGCAGACTGGACCTTTTGGACACTGTATTCATGTAACTGCAAGG 1457
Db 1201 AAGAGATTTACAGGAGACTGGGCTTTTGGACACTGTATTTCTTTACTGTCAAGG 1260
Oy 1458 GGAGGGGCTTCGATCCAGACACAGAGACTGTACTCAGGGGATGAGAAACCTTGACATC 1517
Db 1261 GGAGGGGCTTCGATCCAGACACAGAGATGTTATTACAGGGATGAGAAATCTGACAT - 1319
Oy 1518 CCTAGTGTGCTGACTGCCCCATTGTTTCTACACAGATCCACAAGACCCCGCAGCTGC 1577
Db 1320 --TGAGTGTGCTGACTGCCCCAATTGTTTCTACAAACATCCGACAGACCCCGCAGCTGC 1377
Oy 1578 AAGCGTGGCCCTTCGCAATGGGTTGACGTGCTCCGAGATGGCTGACAGACAGAGAGTG 1637
Db 1378 AAGCGATGCTCCCTGCTCATACGGGTTACGCTGTCAAGATGCGGAGACGAGAGAGTG 1437
Oy 1638 GTGTCAATTAACCTGCCCCAGAGGTGTCACTGATCCGCGTGTGAGCTCTGTGTGATGGC 1697
Db 1438 GTGTCAATTAACCTGCCCCAGAGGTGTCAACCGGTGCGGCTGTGAGCTCTGTGTGATGGC 1497
Oy 1698 TATTTTGGGGAACCCCTTGGGGAACGTGCCCCAGTGAAGCCCTGTACAGCTGTGACGTG 1757
Db 1498 TACTTTGGGGAACCCCTTGGTGTGAACATGGCCAGTGAAGCCCTGTACAGCCCTGTCAATGC 1557
Oy 1758 AACAAACAGTGGAGCCCTAGTGCCTCCGGAACGTGTACCCGCTGACAGAGAGGTGCTG 1817
Db 1558 AACAAACAGTGGAGCCCCAGTGCCTCTGGGAATGTGACCGGCTGACAGGAGGTGTTG 1617
Oy 1818 AAGTCAATCCAAACACAGCTGGGGTCCACTGTACACAGTGCAAAGCAGGCTACTATAGG 1877
Db 1618 AAGTCAATCCAAACACAGCGCGCATCTACGTGACACAGTGCAAAGCAGGCTACTGTGGG 1677
Oy 1878 GAACCGTGGCTCCCAATCCAGCAGACAGATGTGAGCTTGCATCACTGCACCCAGTGGGC 1937
Db 1678 GAACCGTGGCTCCCAACCCAGCAGACAGATGTGAGCTTGCATCACTGCACCCAGTGGGC 1737
Oy 1938 TCGGAGCGCTGTGGAGTGTGGAAGTGTGAGGAGCTGTGTTTCAAGCCAGGCTTGTGGTGGC 1997
Db 1738 TCGAGCGCTGTAGAGTGTGGAAGTGTGAGGAGCTGTGTTTCAAGCCAGGAGTTTGTGGC 1797
Oy 1998 CTCAGCTGTGAGCATGTGCGCACTGACAGCCTGTCCAGCTTCTATTAATCAAGTAAAGTT 2057
Db 1798 CCCAAGTGTGAGCATGTGAGCAT--CAGCTGTCCAGTGTCTTAATCAAGTAAAGTT 1854
Oy 2058 CAGATGATCACTTATGACAGCAGCTCCAGATCCTGAGGCGCTGTATTCGAAGCTCAG 2117
Db 1855 CAGATGATCACTTATGACAGCAGCTCCAGATCCTGAGGCGCTGTATTCGAAGCTCAG 1914
Oy 2118 GG-----TGGAGCAGTACCCCAAGCAGAGCTGGAAAGCAGAGTGCAGCAGCTGAGCAG 2171
Db 1915 GGTGTGATGAGTATGTAATCTGTATACAGAGCTGGAAAGCAGAGTGCAGCAGCTGAGCAG 1974
Oy 2172 GCCCTTGGGCAATTTCTGAGAGAAAGCCAGATTTCAAGATGCTGTTAGATCCTTCAT 2231
Db 1975 GCCCTTGGGCAATTTCTGAGAGATGCCCCAGATTTCAAGAGTGTGAGCAGATCCTTGT 2034
Oy 2232 CTCGGGTTGGCCAAAGGACATCAGAGATAGCTACCGGAGCCGCTGTGATGACCTC 2291
Db 2035 CTCAGTGTGGCCAAAGGTGAGGACCAAGAGACAGCTACCGAAGCCGCTGTGATGACCTC 2094
Oy 2292 AAGATGACTGTGGAAGAGTTCGGGCGCTGGGAGTCAAGTATCAAGAACCAAGTTCAGAT 2351
Db 2095 AAGATGACTGTGGAAGAGTTCGGGCTGTGGAAAGTCAAGTACCGAAGCCGATGGGAT 2154
Oy 2352 ACTGCAAGCTCATCTCAGATGCGCTGAGCCTGGAAGAGTGAAGCTTCCCTGCA 2411
Db 2155 ACTGCAAGGCTCATCTCAGATGAGCTGAGCCTGGGAGAGAGTGAAGCTTCCCTGGA 2214
Oy 2412 AACACCAATTCCTCTTACAGACATCTAGTGGGCGCAATGCGCTTTAAAGTGTGGCT 2471
Db 2215 AACACTAACATTCCTCTTACAGACACTACGTGGGCGCAATGCGCTTTAAAGTGTGGCT 2274

QY 2472 CAGAGGCCAGGATTGGCAGACAGCCATGTTCACTCAGCCAGTAAACATGAGCAACTG 2531
 DB 2275 CAGAGGCCACAGAGATTAGCAGAAAGCAGCTTGAGTCAGCCAGTAAACATGAGCAACTG 2534
 QY 2532 GCAGAGAAACCCAGAGATTTCGCAAGAGCTATGTCAGTGGTGGCCAGGCTCTGCGAG 2591
 DB 2335 ACAGAGAAACCTAGAGCTATTCGCAAGAGCTATGTCAGTGGTGGCCAGGCTCTGCGAG 2594
 QY 2592 GAAGAG-----GCGGAAGCCGAGCCCTGAGCAGAGCCCTGGTGCAGAGGCTTGGGA 2645
 DB 2395 GAAGAGTCGGAAGCCGAGAGCCGAGCCGAGGCTGCTGCTGGTGCAGAGGCTTGGGA 2454
 QY 2646 AAATTCAGAGAAACCTAAATCTCTGGCCAGAGATTGTCAGAGGAGCCAGCAACCGAC 2705
 DB 2455 AAATTCAGAGAAACCTAAATCTCTGGCCAGAGATTGTCAGAGGAGCCAGCAACCGAG 2514
 QY 2706 ATGGAGCAATAGGCTTTATCAGCAATAGTCTCAGCTTCTCAATCCGCTCAGATT 2765
 DB 2515 ATGGAGCAATAGGCTTTATCAGCAATAGTCTCAGCTTCTCAATCCGCTCAGATT 2574
 QY 2766 CAGGAGTCATAGTATGATCTCTCAGAGT---AGAAAGCAGAGAGGCTCAGACAAAAAGCT 2822
 DB 2575 CAGGAGTCATAGTATGATCTCTCAGAGT---AGAAAGCAGAGAGGCTCAGACAAAAAGCT 2834
 QY 2823 GATTCTCTCAAAACGCTGACTAAGCATATGATGATGATGATGATGATGATGATGATGAT 2882
 DB 2635 GATTCTCTCAAAACGCTGACTAAGCATATGATGATGATGATGATGATGATGATGATGAT 2694
 QY 2883 CTGGGAAACCTGGGAAAGAGAAAGAACCCGAGCCTTTCAGAGTAAAGAAAGTGGAGACAG 2942
 DB 2695 CTGGGAAACCTGGGAAAGAGAAAGAACCCGAGCCTTTCAGAGTAAAGAAAGTGGAGAGAG 2754
 QY 2943 ACATCAGATCAGCTGCTTCCGTCGCAACCTTCTTAAAGCAGAGCCAGAGAGCACTA 3002
 DB 2755 AATTCAGATCAGCTGCTTCCGTCGCAACCTTCTTAAAGCAGAGCCAGAGAGCACTG 2814
 QY 3003 AGTATGGGCAATGCCACTTTTATGAGATTGAGAACCTTCTTAAAGTCTCAGAGAGTTT 3062
 DB 2815 AGTATGGGCAATGCCACTTTTATGAGATTGAGAACCTTCTTAAAGTCTCAGAGAGTTT 2874
 QY 3063 GACCTCAGGTTGGAGATAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3122
 DB 2875 GACCTCAGGTTGGAGATAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2934
 QY 3123 ATCAGCCAGAGAGTTCAGAGTTCAGTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3182
 DB 2935 ATCAGCCAGAGAGTTCAGAGTTCAGTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2994
 QY 3183 AGTCTGCTGCCAGAGCCAG 3242
 DB 2995 AGGCTGCTGCTGATGCACAG 3054
 QY 3243 GCGAAGTGAAG 3302
 DB 3055 AGGAGATTAAG 3114
 QY 3303 GCGTTGGCATGAG 3362
 DB 3115 GCGTTGGCATGAG 3174
 QY 3363 GAGCTTCAG 3422
 DB 3175 GAGCTTCAG 3234
 QY 3423 GCGAGAGCCCAAGAGATTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3482
 DB 3235 ACAGAGAGCCAG 3294
 QY 3483 CTCACACATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3542
 DB 3295 CTCACACATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3354

QY 3543 AGGCTGATCTTACTGGAGCAGAGCTTTTCGAGCCAGAGCTAGATCAACAGCCAGCTA 3602
 DB 3355 GGGCTGCTTACTGGAGCAGAGCTTTTCGAGCCAGAGCTAGATCAACAGCCAGCTA 3414
 QY 3603 CGGCTTGTATGTCAGAGCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3662
 DB 3415 CGGCTTGTATGTCAGAGCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3474
 QY 3663 CTGAGAGCTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3722
 DB 3475 CTGAGAGCTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3534
 QY 3723 AACCTGCCCCGGGCTGCTACAAATACCCAGAGCTTGTGAGCAGACGTGA 3770
 DB 3535 AACCTGCCCCGGGCTGCTACAAATACCCAGAGCTTGTGAGCAGACGTGA 3582

RESULT 9
 AAC83732
 ID AAC83732 standard; cDNA; 3620 BP.

XX AAC83732;
 AC 02-MAR-2001 (first entry)
 DE Human laminin 5 cDNA, SEQ ID NO: 31.
 XX Human: laminin 5; vulnery; antiulcer; antiinflammatory; antidiabetic;
 KM cell adhesion promoter; wound healing; ulcers; burn; skin graft;
 KM periodontitis; gingivitis; Type I diabetes; angiogenesis regulation; ss.
 OS Homo sapiens.
 PN MO200066731-A2.
 XX 09-NOV-2000.
 PD 28-APR-2000; 2000MO-US11459.
 XX 30-APR-1999; 99US-0131720.
 PR 21-AUG-1999; 99US-0149738.
 PR 24-SEP-1999; 99US-0155945.
 XX (BIOS-) BIOSTARDUM INC.
 PA Boutaud A;
 PI WPI: 2000-687538/67.
 DR P-PSDB; AAB48471.
 DR Laminin 5-expressing cells, used to accelerate wound healing associated
 PT with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
 PT burns, acute wounds and skin grafts -
 XX Claim 4; Page 204-209; 232pp; English.
 PS The present sequence encodes a laminin 5 chain polypeptide. Recombinant
 CC laminin 5-expressing cells are used to accelerate wound healing,
 CC especially diabetic foot ulcers, venous ulcers, pressure sores, skin
 CC surgery, burns, acute wounds, skin grafts, corneal ulcerations,
 CC gastro-intestinal ulcers, periodontitis, and gingivitis. They are also
 CC used to improve the biocompatibility of medical devices, and to promote
 CC cell adhesion to a surface. They can be used for the ex vivo treatment
 CC of Type I diabetes. Laminin can also be used to regulate angiogenesis.
 CC The cell line produces and secretes recombinant heterotrimeric laminin,
 CC whereas prior art cell lines have been created that produce but do not
 CC secrete only one or two chain laminins.
 XX Sequence 3620 BP; 959 A; 862 C; 1040 G; 759 T; 0 other;

Query Match 72.2%; Score 2880.8; DB 21; Length 3620;
 Best Local Similarity 88.6%; Pred. No. 0;
 Matches 3184; Conservative 0; Mismatches 387; Indels 21; Gaps 5;

OY	261	ACCTCCGGGAGGAGAGTCTGTGATTGCAACGGGAATCGAAGCAATGCATCTTTGACAG	320
Db	1	ACCTCCAGGAGGAGAGTCTGTGATTGCAATGGGAATCGAGCACTGTAATCTTGTATCG	60
OY	321	GAACTTCACAAACAGACAGAAATGATTCGGCTCCCTCACTGTAATGACAACTGAT	380
OY	381	GGCATCCACTCGAGAGGTGCAAGGCAAGATTTTACCAACAGAGAAAGGACCGCTGT	440
Db	121	GGCATTCACCTGCAGAAATGCAAGAATGGCTTTTACCGGACACAGAAAGGACCGCTGT	180
OY	441	TTACCCCTGCATTTGTAACCTTAAGAGTTCTCTTACGCTCGATGTGACAACTCTGACGG	500
Db	181	TTGGCTTCGAATTTGTAACCTCCAAAGGTTCTCTTAAGTGTGATGTGACAACTCTGGACG	240
OY	501	TGCAGCTGTAAAGCCAGGTGTGACAGAGAACAGGTGTGACCGATGTGCGCCGGTTCCAC	560
Db	241	TGCAGCTGTAAACCAAGGTGTGACAGAGAACAGGTGTGACCGATGTGCGCCGGTTCCAC	300
OY	561	ACACTCACTGATGCTGGGTGCGCCCAAGACAAAGGCTGTAAGACTCCAAAGTACTGT	620
Db	301	ATGCTCAACGATGCGGGGTGCAACCAAGACAGACTGTGTAAGTCTCAAGTGAAGTGT	360
OY	621	GACCCAGTGTGCATCTCAGGGGCCCTGTGATCTAGGCCCTGTGTGTGCAAGCCGCTGTG	680
Db	361	GACCCAGTGTGCATCTCAGGGGCCCTGTGATCTAGGCCCTGTGTGTGCAAGCCACTGTT	420
OY	681	ACTGAGAGAGCCCTGTGATAGTGTGTCAGACAGTGTCTATACACCTGATGGGGAACCTT	740
Db	421	ACTGAGAGAGCCTGTGATAGTGTGTCAGAGTTTACTTAATCTGGAATGGGGGAACCTT	480
OY	741	CAGGGCTGTACCCAGTGTCTTGTCTATGGGCAATTCGCGAGCTGCGACAGCTCTGGGAC	800
Db	481	GAGGGCTGTACCCAGTGTCTTGTCTATGGGCAATTCAGCGAGCTGCGGAGCTCTGACAA	540
OY	801	TACAGTGTCCAAATAATCATCTGCGCTTCCATCAAGATGTGAATGCTGGAAAGCTGTG	860
Db	541	TACAGTGTCCAAATGATACCTCTACCTTTTCAATCAAGATGTGAATGCTGGAAAGCTGTG	600
OY	861	CAAGAAAGGGGTCTCTGCAAAAGCTCCAGTGTGTCACAGCCGCACTGGGATATATTAGC	920
Db	601	CAAGAAATGGGTCTCTGCAAAAGCTCCAAAGTGTGTCACAGCCGCACTGAAGTGTTHAGC	660
OY	921	TCAGCAGAGCATCAGACCCGTGTCTATTTTGTAGCTCCTGCCAAATTTCTTGGGAATCA	980
Db	661	TCAGCAGCAGCATAGACCCGTGTCTATTTTGTAGCTCCTGCCAAATTTCTTGGGAATCA	720
OY	981	CAGGTGACATACGGGCAAAAGCTATCTTTGATCTACGATCGATGGGGAAGGACGACAC	1040
Db	721	CAGGTGACATATGGGCAAAAGCTATCTTTGATCTACGATCGATGGGGAAGGACGACAC	780
OY	1041	CCATCTGCGCATGAGAGTATCCTGTGAAAGTGTGTCTACAGGATCACAGCTCCCTTGATG	1100
Db	781	CCATCTGCGCATGAGATGATCTGTGAAAGTGTGTCTACAGGATCACAGCTCCCTTGATG	840
OY	1101	CCACTTACGACACACTGCTTTGTGTGGATACACAAAGACTTACACATTAGATTAATGAA	1160
Db	841	CCACTTACGACACACTGCTTTGTGTGGATACACAAAGACTTACACATTAGATTAATGAG	900
OY	1161	CATCCAAAGCAATATTTGGAGCCCCCAGGTAAAGTACTTTGATATCGGAGTTTACTGGG	1220
Db	901	CATCCAAAGCAATATTTGGAGCCCCCAGGTAAAGTACTTTGATATCGAAGTTTACTGGG	960
OY	1221	AACCTCACAGCCCTGCGGATCCGAGTACTTACGAGAGATACAGTACTGGGTACTTGAC	1280
Db	961	AATCTCACAGCCCTCCGATCCGAGTACTTACATATGAGAGATACAGTACTGGGTACTTGAC	1020
OY	1281	AAGGTGACCTGATTTGAGCCCCCCTTTCTGTGAGGCCAGCGCCCTGGGTTGACAA	1340
Db	1021	AATGTGACCTGATTTGAGCCCCCCTTTCTGTGAGGCCAGCACCCCTGGGTTGAAACAG	1080

QY	1341	TGTTATAGCCCTGTTGGCTACAAAGGGGCACTTGTGCCAGATTTGGCTTCGGGCTACAAA	1400
Db	1081	TGTTATAGTCTCTGTTGGGTACAAAGGGGCAATTTCTGCCAGATTGTGCTTCTGGCTACAG	1140
QY	1401	AGAAATTACAGCACTGGGACCTTTTGGACACTGTATTCATATGTAACGTCCAAAGGGGA	1460
Db	1141	AGAAATTACAGCACTGGGACCTTTTGGCACCCTGTATTCTTGTAACTGTCAAGGGGA	1200
QY	1461	GGGGCTTGCATCCAGACAGGAGACTGTACTGAGGGGATGAGAACCTTGACATCCCT	1520
Db	1201	GGGGCTTGTATCCAGACAGGAGATTGTTATTACAGGGAGTGAATTCCTGACAT---T	1257
QY	1521	GAGGTGCTACAGTGGCCCATTTGGTTCTTCAACGATCCCAAGACCCCGACGTGCAAG	1580
Db	1258	GAGGTGCTGACTGGCCCAATTTGGTTCTCAACGATCCCAAGACCCCGACGTGCAAG	1317
QY	1581	CCGTGCCCTGTGCAATGGGTTCAGCTGCTCCGTGATCCCTGAGACAGAGAGGTGTG	1640
Db	1318	CCATGTCCCTGTCTAATACGGGTTACAGTGTCTAGTATGTCGGAGCCGAGAGAGGTGTG	1377
QY	1641	TGCAATTAACTGCCCCCAGGGGTCTCATCTGGTCCCGCTGTGACCTGTGTCTGATGGCTAT	1700
Db	1378	TGCATTAACGTCCCTCCCGGGGTACCCGGGCCCGGTGTGACCTGTGTGATGGGTAC	1437
QY	1701	TTTGGGGAACCCCTTCGGGGAACTGGGCCCACTGAGGSCCTTGTACGCCCTGTCAATGCAAC	1760
Db	1438	TTTGGGGAACCCCTTTGGTGAACATGGGCCCACTGAGGSCCTTGTACGCCCTGTCAATGCAAC	1497
QY	1761	AACAAGCTGACCCCTAGTGCCTCCGGGAACGTGTACCGCTGACAGGCAAGGTGTCTGAAG	1820
Db	1498	AACAATGTGGACCCCACTGCTCTCGGGAATTGTGACCGGCTCAACAGGCGTGTGTGAAG	1557
QY	1821	TGCATTCACAACAGATGGGGGTGCCACTGTGAACACTGTGAAAGACAGGCTACTATGGGAC	1880
Db	1558	TGTTATCCACAAACAGCCGACACTTACTGTGACCACTGTCAAAAGCAGAGCTACTTGGGGAC	1617
QY	1881	CCGTTGGCTCCCAATCCAGCAGCAAGTGTGAGCTTGCACACTGCACCACTGGGGCTCG	1940
Db	1618	CCATTGGCTCCCAACCCAGCAGACAAGTGTGACGCTTGCACATGTAAACCCATGGGCTCA	1677
QY	1941	GAGCCTGTGAGAGTGTCAAGTATGACAGTGTGTTTGAACCAAGGCTTGGTGGCCCTC	2000
Db	1678	GAGCCTGTGAGAGTGTCAAGTATGACACTGTGTTTGAAGCAGAGATTTGGTGGCCCTC	1737
QY	2001	AGCTGTAGCATGGGCACTGACACAGCTGTCCAGCTTGTCTAATATCAAGTCAAGTTTAC	2060
Db	1738	AACGTGTAGCATGGGCACTT---CACTGTCCAGCTTGTCTAATATCAAGTCAAGTTTAC	1794
QY	2061	ATGATATCAATTTATGACAGAGCTTCCAGATCTTGGAGGCCCTGATTTCCAGGCTCAGGG-	2119
Db	1795	ATGATATCAATTTATGACAGAGCTTCCAGATATGAGAGGCCCTTATTTCAAAGGCTCAGGGT	1854
QY	2120	-----TGGAGCAATGCCAACGAGAGCTGGAAGGAGGACAGATGACAGAGGCTGACAGGCC	2174
Db	1855	GGTATGTGAGTATGACTGTATACAGAGCTGTGAAGGACAGAGATGACAGAGGCTTACAGAGGCC	1914
QY	2175	CTTCGGGACATTTGAGAGAGGCCAGATTTCAACAAGATGCTGTAGATCTTCAATCTC	2234
Db	1915	CTTCAGGACATTTCTGAGAGATGTGCCAGATTTCTGAAGAGTGTCAAGAGATCCCTTGTGCTC	1974
QY	2235	CGGGTGGCCAAAGGACAGACTCAAGAGAAATAGCTATCCGGGACCGCGCTGGATATAGCTCAAG	2294
Db	1975	CAGTTGGCCAAAGGTGAGAGGACCAAGAGAACAGCTTACCAAGGCCGCGCTGGATATAGCTCAAG	2034
QY	2295	ATGACTGTGGAAGAGTTCCGGGCTTGGGCACTTACCAAGAACCAAGATTCAGATCTACT	2354
Db	2035	ATGACTGTGGAAGAGTTCCGGGCTTGGGCACTTACCAAGAACCAAGATTCAGATCTACT	2094
QY	2355	CGCAGGCTCATCTAGATGAGCCCTGAGAGCTGTGAGAGAAAGTGAAGCTTCCTGCAAAAC	2414
Db	2095	CACAGGCTCATCTAGATGAGCTGTGAAGCTGTGGCAAGAAAGTGAAGCTTCCTTGGGAAAC	2154
QY	2415	ACCAACAATTCCTCTTAGAGCACTACGTGGGGGCCAAATGGCTTTAAAAGTGTGGCTAC	2474

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Db 2155 ACTACATCTCTGCTGAGACCACTACGTGGGGCCAAATGCTTTAAATCTGGCTCAG 2214
QY 2475 GAGGCCACGAGATTGGCAGACCATGTTCACTACAGCCAGTAACATGAGCACTGGCA 2534
Db 2215 GAGGCCACGAGATTGAGCAAGCCAGCTTGAATGAGCCAGTAACATGAGCACTGGCA 2274
QY 2535 AAGAAACCCAGAGATTCTCAAGAGCTGATGTCTAGTGGCGGAGGCTCTGACGAA 2594
Db 2275 AGGAAACTGAGGCTATCTCAAAAGCCCTCACTGATGGTGGCAAGGCCCTGCATGAA 2334
QY 2595 GGAG-----GCGGAACCGCAGCTTGAGAGCCCTGGTTCGAAAGGCTTGGGAAA 2648
Db 2335 GAGGTGCGAAGCCGAGACGGTACCGCGAGCTGTGTGCGAAGGCTTGGGAAA 2394
QY 2649 TTGAGAAAACCTAAATCTCTGGCCAGAGATTGTGCGAGGAGGCCAGCAACCGACAT 2708
Db 2395 TTGAGAAAACCAAGTCTCCCTGGCCAGCAATTTGACAAAGGAGGCCACTCAAGGGAA 2454
QY 2709 GAAGCAGATAGTCTTATACAGCATAGTCTCCACCTTCTCAATTCCTGCTCAGATT 2768
Db 2455 GAAGCAGATAGTCTTATACAGCATAGTCTCCACCTTCTCAATTCCTGCTCAGATT 2814
QY 2769 GAGTCAATATAGTCTTCTGCAAGT---AGAAAGCCAGAGGCTCAGACAAAAGCTGAT 2825
Db 2515 GAGTCTGATAGTCTTCTGCAAGT---AGAAAGCCAGAGGCTCAGACAAAAGCTGAT 2574
QY 2826 TCTCTCAAAACCGTGTGACTTAAGCATATGATGATGATGATGATGATGATGATGAT 2885
Db 2575 TCACTCTCAAGCTCGTGAACCAAGCATATGATGATGATGATGATGATGATGATGAT 2634
QY 2886 GGAACCTGGAGAGAAACCCGCGACCTCTTACAGATGAGAAAGAAAGAGAGACAGACA 2945
Db 2635 GGAACCTGGAGAGAAAGAGACAGACAGCTCTTACAGATGAGAAAGAAAGAGAGAGAA 2694
QY 2946 TCAATCAGCTGCTTTCCCTGCGCAACCTTGTAAAGAGAGAGAGAGAGAGAGAGAG 3005
Db 2695 TCAATCAGCTGCTTTCCCTGCGCAACCTTGTAAAGAGAGAGAGAGAGAGAGAGAG 2754
QY 3006 ATGGGCATGCCACTTTTATGAGATGAGAAATCTTAAAGATCTCAGAGATTGAC 3065
Db 2755 ATGGGCATGCCACTTTTATGAGATGAGAAATCTTAAAGATCTCAGAGATTGAC 2814
QY 3066 CTCAGAGTTGAGATTAAGAGCAAGAGCTGAAAGAGCCATGAGAGACTCTCTACATC 3125
Db 2815 CTCAGAGTTGAGATTAAGAGCAAGAGCTGAAAGAGCCATGAGAGACTCTCTACATC 2874
QY 3126 AGCCAGAGTTGAGATGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGC 3185
Db 2875 AGCCAGAGTTGAGATGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGC 2934
QY 3186 GCTGCTGCCAGCCAGAGAGGCAAGATGACAGAGGAGCCCTGAGATCTCTGCG 3245
Db 2935 GCTGCTGCCAGCCAGAGAGGCAAGATGAGAGGAGCCCTGAGATCTCTGCG 2994
QY 3246 AATATATGAGAGAGATGAGAGCTCTGACTTGAAGCCATGATGACAGAGATGAGCC 3305
Db 2995 GATATATGAGAGAGATGAGAGCTCTGACTTGAAGCCATGATGACAGAGATGAGCC 3054
QY 3306 TTGGCATGAGAGAGAGGAGCTGACCTGTAAGAGATGAGTGAAGAGAGAGAGAGAG 3365
Db 3055 TTGGCATGAGAGAGAGGAGCTGACCTGTAAGAGATGAGTGAAGAGAGAGAGAGAG 3114
QY 3366 CTGTCAAGAGAGAGAGAGGATTTGACATGATGAGAGCCAGTGCAGATGATGATGCA 3425
Db 3115 CTGTCAAGAGAGAGAGGATTTGACATGATGAGAGCCAGTGCAGATGATGATGCA 3174
QY 3426 GAGGCCCAAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3485
Db 3175 GAGGCCCAAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3234
QY 3486 AACACATTTGATGAGATCTCTACACCTTAATGAGCCAGCTGCGAGTGTGATGAGAGAG 3545
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Db 3235 AACACATTTAGAGAGGCTCTCTGATCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 3294
QY 3546 CTGATCTTACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3605
Db 3295 CTGATCTTACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3354
QY 3606 CCCTGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3665
Db 3355 CCATGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3414
QY 3666 GAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3725
Db 3415 GAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3474
QY 3726 CTGCCCCCGGCTGCTCAATATACAGAGCTCTTGAAGCAAGAGAGAGAGAGAGAGAG 3785
Db 3475 CTGCCCCCGGCTGCTCAATATACAGAGCTCTTGAAGCAAGAGAGAGAGAGAGAGAG 3534
QY 3786 TTCTCAACCAAGGCTTCTGGGATTCAGACCTAGCTGCTTGAAGATTTCTCA 3837
Db 3535 TTCTCAACCAAGGCTTCTGGGATTCAGATCTCAGGCTCGGAGAGCATGTCA 3586

RESULT 10
AAC83730
ID AAC83730 standard; cdna; 5020 BP.
XX
AC AAC83730;
XX
DT 02-MAR-2001 (first entry)
XX
DE Human laminin 5 cDNA, SEQ ID NO: 27.
XX
KW Human; laminin 5; vulnerability; antifungal; anti-inflammatory; antidiabetic;
KW cell adhesion promoter; wound healing; ulcers; burn; skin graft;
KW periodontitis; gingivitis; type I diabetes; angiogenesis regulation; ss.
XX
OS Homo sapiens.
XX
PN WO200066731-A2.
XX
PD 09-NOV-2000.
XX
PE 28-APR-2000; 2000MO-US11459.
XX
PR 30-APR-1999; 99US-0131720.
PR 21-AUG-1999; 99US-0149738.
PR 24-SEP-1999; 99US-0155945.
XX
PA (BIOS-) BIOSSTATUM INC.
XX
PI Boudaud A;
XX
DR WPI: 2000-687538/67.
XX
DR P-PDB; AAB48469.
XX
PT Laminin 5-expressing cells, used to accelerate wound healing associated
PT with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
PT burns, acute wounds and skin grafts -
XX
PS Claim 4; Page 185-191; 232pp; English.
XX

The present sequence encodes a laminin 5 chain polypeptide. Recombinant
CC laminin 5-expressing cells are used to accelerate wound healing,
CC especially diabetic foot ulcers, venous ulcers, pressure sores, skin
CC surgery, burns, acute wounds, skin grafts, corneal ulcerations,
CC gastro-intestinal ulcers, periodontitis, and gingivitis. They are also
CC used to improve the biocompatibility of medical devices, and to promote
CC cell adhesion to a surface. They can be used for the ex vivo treatment
CC of Type I diabetes. Laminin can also be used to regulate angiogenesis.
CC The cell line produces and secretes recombinant heterotrimeric laminin,
CC whereas prior art cell lines have been created that produce but do not
CC secrete only one or two chain laminins.
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XX Sequence 5020 BP; 1329 A; 1170 C; 1333 G; 1188 T; 0 other;
SQ
Query Match 72.2%; Score 2879.2; DB 21; Length 5020;
Best Local Similarity 88.6%; Pred. No. 0;
Matches 3183; Conservative 0; Mismatches 388; Indels 21; Gaps 5;

QY 261 ACCTCCGGGAGGAGTCTGTGATTCGACCGGAGTCCAGGCAATGCATCTTTGACCAG 320
DB 1 ACCTCCGAGGAGGAGTCTGTGATTCGACCGGAGTCCAGGCAATGCATCTTTGACCAG 60
QY 321 GAATTCACAAACAGACAGAAATGATTCGCTGCTCAACTGCAATGACACACTGAT 380
DB 61 GAATTCACAGACAAACTGTAAATGATTCGCTGCTCAACTGCAATGACAACTGAT 120
QY 381 GGCATTCACGCGAGGAGTGCAGGCAAGATTTACGACAGAGAGAAAGGAGCGGTGT 440
DB 121 GGCATTCACGCGAGGAGTGCAGGCAAGATTTACGCGGACAGAGAAAGGAGCGGTGT 180
QY 441 TTACCTTCGCAATTTGTAATCTTAAAGTTCCTTACGCTCGATGTCACAACTTCGACGG 500
DB 181 TTGCTTCGCAATTTGTAATCTTAAAGGTTCTCTTGTAGTGTGATGACAACTTCGACGG 240
QY 501 TGCAGCTGTAAAGCCAGGTGTGACAGAGACAGGTGTACGATGTTCGCCGCTTCAC 560
DB 241 TGCAGCTGTAAACAGGTGTGACAGAGCCAGATGTCCGATGTTCGCCAGGCTTCAC 300
QY 561 ACATCTACTGATGCTGGGGTGGCCCAAGACCAGGCGTGAAGTCCAAAGTGTGACTGT 620
DB 301 ATGCTCACGATGCTGGGGTGCACCCCAAGACCAGACTGTGACTCCAAAGTGTGACTGT 360
QY 621 GACCCAGCTGGCATCTAGGGCCCTGTGACTCAGGCGGTGTCTGTGCAAGCCGCTGTC 680
DB 361 GACCCAGCTGGCATCTGAGGGCCCTGTGACGCGGGCCGCTGTGTGCAAGCCGAGCTT 420
QY 681 ACTGGAAGCGCTGTGATAGTGTGACAGAGTACTATCACTCTGATGGGGAACCTT 740
DB 421 ACTGGAAGACCTGTGATAGTGTGACAGTACTATCACTCTGATGGGGAACCTT 480
QY 741 CAGGCTGTATACCGAGTGTGTGCTATGGGCAATCCGACGTGCGAGCTGGGGAG 800
DB 481 GAGGCTGTATACCGAGTGTGTGCTATGGGCAATCCGACGTGCGAGCTGTGCAAA 540
QY 801 TACAGTGTCCATAAATCATCTCTGCCCTTCATCAAGATGTGATGGCTGGAAGGCTGTC 860
DB 541 TACAGTGTCCATAAATCATCTCTACCTTCATCAAGATGTGATGGCTGGAAGGCTGTC 600
QY 861 CAAAGAAAGCGGTCTCTGCAAAAGCTCCAGTGTGACAGGCCCATCGGATATATTAGC 920
DB 601 CAAAGAAATGGGTCTCTGCAAAAGCTCCAAATGTGACAGCGCATCAAGATGTGTTAGC 660
QY 921 TCACAGCAGCATGAGACCTGTCTAATTTGTAGTCTGCGCAATTTCTTGGGAAATCA 980
DB 661 TCACAGCCCAACATGATCTGTCTAATTTGTGCTCTGCGCAATTTCTTGGGAAATCA 720
QY 981 CAGGTGAGCTACGGGCAAGCCTATCTTTGACTACCTGTGATGAGGAGGAGCGACAC 1040
DB 721 CAGGTGAGCTATGAGGCAAGCCTGTGCTTGTACTACCTGTGAGAGAGGAGCGACAC 780
QY 1041 CCATCTGCCATGAGCTGATCTCTGAGAGGTGCTGCTACGAGATCAAGCTCCCTGATG 1100
DB 781 CCATCTGCCATGAGTGTATCTCTGAGAGGTGCTGCTACGAGATCAAGCTCCCTGATG 840
QY 1101 CCATCTGCAAGACACTGCTGTGGGAGTCAACCAAGATTTACACTTACATTAATAA 1160
DB 841 CCATCTGCAAGACACTGCTGTGGGAGTCAACCAAGATTTACACTTACATTAATAA 900
QY 1161 CATCCAAAGCACTAATTTGAGGCCCGCAGCTAAGTTACTTGAATCGAGGTTACTGCGG 1220
DB 901 CATCCAAAGCACTAATTTGAGGCCCGCAGCTGAGTTACTTGAATCGAGGTTACTGCGG 960
QY 1221 AACCTCACAGCCCTGCGGATCCGAGCTACCTACGAGAGATACAGTACTGGGTACATTGAC 1280
DB 1221 AACCTCACAGCCCTGCGGATCCGAGCTACCTACGAGAGATACAGTACTGGGTACATTGAC 1280

DB 961 AATCTCACAGCCCTCCGATCCGAGCTACATATGAGAAATACGACTGGGTACATTGAC 1020
QY 1281 AACGTACCTTGATTTGAGCCCGCCGTTCTTGAGCCCGCAGCGCCCTGGGTGAACAA 1340
DB 1021 AATGTACCTTGATTTGAGCCCGCCGTTCTTGAGCCCGCAGCGCCCTGGGTGAACAA 1080
QY 1341 TGTGTATGCCCTGTTGCTACAGAGGCGAGTCTGCGACAGATTGTGCTTCGCTACAAA 1400
DB 1081 TGTATATGCTCTGTTGGGTACAAAGGGCAATTTGCCAGAGATTGTGCTTCGCTACAA 1140
QY 1401 AGAATTCAGCACAACCTGGGACCTTTTGGCACCTGTATTCATATTACTGCAAGGGGA 1460
DB 1141 AGAATTCAGGAGACCTGGGACCTTTTGGCACCTGTATTCATATTACTGCAAGGGGA 1200
QY 1461 GGGGCTCGCATTCAGACACAGAGAGACTGTACTCAGGGAGTGAAGAACCCGACATCCCT 1520
DB 1201 GGGGCTGTGATTCAGACACAGAGAGATTGTTATTCAGGGAGTGAAGAACCTCGACAT -T 1257
QY 1521 GAGTGTGCTGACTGCCCCCATTTGTTTACAAAGATCCCAAGACCCCGCAGCTGCAAG 1580
DB 1258 GAGTGTGCTGACTGCCCCCATTTGTTTACAAAGATCCGACAGACCCCGCAGCTGCAAG 1317
QY 1581 CCGTGGCCCTGTGCGCAATGGGTGACGTGCTCCGTGATAGCTGTGAGACAGAGAGAGTGTG 1640
DB 1318 CCATGTCCCTGTCAATACAGGGGTTCAGCTGCTCACTGATTCGAGAGAGAGAGAGTGTG 1377
QY 1641 TGCATTAATCTGCCCCCAGAGGTGTCACTGTGCTGCGCTGTGAGCTGTGATGAGCTAT 1700
DB 1378 TGCATTAATCTGCCCCCAGAGGTGTCACTGTGCTGCGCTGTGAGCTGTGATGAGCTAT 1437
QY 1701 TTTGGGAGCCCTTTCGGGGAAGTGGCCAGTGAAGGCTTGTGACGCTGTCACTGTGCAAC 1760
DB 1438 TTTGGGAGCCCTTTCGGGGAAGTGGGAACATGAGCCCACTGAGAGCTTGTGACGCTGTCAATGTCAAC 1497
QY 1761 AACAACTGAGACCTTACGTGCTCCGCGAAGCTGTGACGCTGTGACAGAGAGTGTCTGAG 1820
DB 1498 AGCATGTGGAAGCCCAAGTGTCTGGGAATTTGATCCGCGTGAAGAGGAGGTGTTGAG 1557
QY 1821 TGCATCCACAACAGCTGGGGTCCACTGTGACAGTGAAGCAGCTTAATATGAGGAG 1880
DB 1558 TGTATCCACAACAGCTGGGGTCCACTGTGACAGTGAAGCAGCTTAATATGAGGAG 1617
QY 1881 CCGTTGGCTCCCAATCCAGACAGCAAGTGTGAGCTTGCACACTGCAAGCCAGTGGCTG 1940
DB 1618 CCATTTGGCTCCCAATCCAGACAGCAAGTGTGAGCTTGCACACTGCAAGCCAGTGGCTG 1677
QY 1941 GAGCCTGTGAGTGTGCAAGAGTGAAGGCAAGTGTGTTGCCAAGCAGAGCTTGGTGGCCTC 2000
DB 1678 GAGCCTGTGAGTGTGCAAGAGTGAAGGCAAGTGTGTTGCCAAGCAGAGCTTGGTGGCCTC 1737
QY 2001 AGCTGTGAGCATGCGGCACTGACAGCTGTCCAGCTGTCTAATTAAGTGAAGTTGAG 2060
DB 1738 AACTGTGAGCATGAGGACTT---CAGCTGTCCAGCTTGTCTAATTAAGTGAAGTTGAG 1794
QY 2061 ATGATGAGTTTATGACAGCTCCAGATCTCGAGGCGCTGATTTGGAAGCTCAGG- 2119
DB 1795 ATGATGAGTTTATGACAGCTCCAGATGAGAGATGAGGCGCTGATTTGGAAGCTCAGG 1854
QY 2120 -----TGAGCAGTACCCCAAGCAGAGCTGGAAGGCAAGATGACAGAGCTGAGAGGCC 2174
DB 1855 GGTGATGAGAGTACCTGATACAGAGCTGGAAGGCAAGATGACAGAGCTGAGAGGCC 1914
QY 2175 CTGGGAGCATTTCTGAGAGAGCCAGATTTACAAAGATGCTGTAGATCTCTCAATGTC 2234
DB 1915 CTTCAGGACATTTCTGAGAGATGCTCAGATTTTACAAAGATGCTGTAGATCTCTCAATGTC 1974
QY 2235 CGGGTGGCAGGCAAGGACTCAAGAGATAGCTACCGGAGCCGCTGAGTGAACCTCAAG 2294
DB 1975 CAGTTGGCAGAGGTGAGAGGCAAGAGAGATACAGAGAGCCGCTGAGTGAACCTCAAG 2034
QY 2295 ATGACTGTGGAAGAGTTCGGGCTGAGGCAAGTACAGTATCAAGAACCAAGTTCAAGATACT 2354
DB 2035 ATGACTGTGGAAGAGTTCGGGCTGAGGCAAGTACAGTATCAAGAACCAAGTTCAAGATACT 2094

QY	2355	CGCAGGCTCATACACACATATGCGCTGAGCTCGAGGGAAGTGAAGCTTCCCTGCAAAAC	2414
Db	2095	CACAGGCTCATACACACATATGAGCTGAGCTCGGCGAAGTGAAGCTTCCCTGGGAAC	2154
QY	2415	ACCAACATATCCCTCTTCAGAGCACATCACTGGGGCCAAATGGCTTTAAAGTGGCTCAG	2474
Db	2155	ACTAACATATCCCTCTTCAGAGCACATCACTAGCTGGGGCCAAATGGCTTTAAAGTCTGGCTCAG	2214
QY	2475	GAGGCCAGAGATTGGCAGACAGCCATGTTCAGTCAGCCAGTAAACATGGAGCACTGGCA	2534
Db	2215	GAGGCCAGACAGATTGGCAGAAAGCCAGCTTAGTCAGCCAGTAAACATGGAGCACTGGCA	2274
QY	2275	AGGGAACATGAGAGCTATTCCAAACAGACCCTCTCAGCTGGTGGCAAGGCCCTGATGAA	2334
Db	2355	GGAG-----GGGGAAGCGGCAAGCCTGGACGAGGCCGTGGTGGCAAAAGGCTTGGGGA	2648
QY	2649	TTGCGAAGAACTCTAATCTCTGTGGCCAGAGATTGTGAGGGAGGCCAGCAACCGACATG	2708
Db	2395	TTGGAGAAACCCAACTCCCTGGCCCGACAGTGTGAACAGGGAGGCCACACCAAGCGAAATT	2454
QY	2709	GAGCAGATAGGCTCTTATCAGCATATAGTCTCCACCTTCATCAATTCGGTCTCAGATTAG	2768
Db	2455	GAGCAGATAGGCTCTTATCAGCAGACAGTCTCCGCCCTCTGGATTAGTGTCTCCGCTTCAG	2514
QY	2769	GGAGTCAATGATCACTCCTTGCAGGT--AGAGCGAAGAGAGCTTCAGCAAAAGCTGAT	2825
Db	2515	GGAGTCAATGATCACTCCTTGCAGGTGGAAGAAAGAGAGATCAACCAAAAGCGGAT	2574
QY	2836	TCTCTCTCAAAACCGGTGACTTAAGATATGGATGTGATCAAGCAGCTGCAAGCAATCTG	2885
Db	2575	TCACCTCTCAAGCTGTGTAAACCAAGCATATGGATGATTCAAAGCGTACCAAAAGATCTG	2634
QY	2886	GGAACCTGGAGAAAGAAACCCGGCAGCTCTTACAGAAATGGAAAGAAATGGAGACAGCA	2945
Db	2635	GGAAACTGGAAAGAAAGAGCAAGCAGCTCTTACAGAAATGGAAAGAAATGGAGAGAGAA	2694
QY	2946	TCAGATCAGCTGCTTCCCGTGGCCAACTGCTTAAAGCAAGCCAAAGAAAGCACTAAGT	3005
Db	2655	TCAGATCAGCTGCTTCCCGTGGCCAACTGCTTAAAGCAAGCAAGAAAGCACTGAGT	2754
QY	3006	ATGGGCAATGCCACTTTTATGAAGTTGAGAACACTTTAAAGAAATCTCAGAGAGTTGAC	3065
Db	2755	ATGGGCAATGCCACTTTTATGAAGTTGAGAAGCATCCTTAAAAOCTCAGAGAGTTGAC	2814
QY	3066	CTGCAGGTTGGAGATTAAGAAAGCAGAGAGCTAAGAGGCCATGAAGAGACTCTCTACATC	3125
Db	2815	CTGCAGGTTGGAGATTAAGAAAGCAGAGAGCTAAGAGAGCCATGAAGAGACTCTCTACATC	2874
QY	3126	AGCCGAGAGTTGCAAGTGGCCAGTACAGCAAGACGAAAGAGAGAGAGAGAGCCCTGGGAGT	3185
Db	2875	AGCCGAGAGTTTTCAGATGATGCCAGTACAGAACCCAGCAGAGAGAAAGAGCCCTGGGAGC	2934
QY	3186	GCTGCTGCCAGCCGCCAGAGGGCAAAAGAAATCAGCCAGAGAGAGGCCCTGAGATCTTGGC	3245
Db	2935	GCTGCTGCTGATGACAGAGGGGCAAAAGAAATGGGCGGGGAGAGGCCCTGGAATCTCCAGT	2994
QY	3246	AAGATAGAAACGAGAGATATGAGAGTCTGACACTTGGAAAGCCATGTGACAGCAGATGGAGCC	3305
Db	2995	GAGATGAAACGAGAGATATGAGAGTCTGACACTTGGAAAGCCATGTGACAGCAGATGGAGCC	3054
QY	3306	TTGGCCATGGAAGAGAGCTGGCCACTGTGAAGAGTGGATGAGAGAGAGTGAAGAGAGAG	3365
Db	3055	TTGGCCATGGAAGAGAGCTGGCCCTCTCTGAAAGTGAATGAGAGAGAGTGAAGAGAGAG	3114
QY	3366	CTGTCAAGGAAGAGCAGAGATTTGACATGATATGGACGCACTGTCAGATGTGTAATGCA	3425
Db	3115	CTGTCAAGGAAGAGCAGAGATTTGACATGATATGGATGTGATGTCAGATGTGTAATGCA	3174

OY	3426	GAGGCCCAAGATGTGAAACAGAGCCAAAGATCGTGGATGTAGATCCAGACACACTC	3485
Db	3175	GAAAGCCCAAGAGTTGATACCGAGAGCCAAAGACGTGGGGTTTACATTCACAGACACTC	3234
OY	3486	AACACATTGGATGGCATCTCTACACTTAATTAACAGCCTCGGACAGTGTGGATGAAGAGAGG	3545
Db	3235	AACACATTAGAGGGCTCTCTCATCTGTATGAGACCACTCTCAGTGTATGATGAAGAGGGG	3294
OY	3546	CTGATCTTACTGGAGACAGAGCTTTTCCGAGCCAGACTCAGATTCACAGCCAGCTACGG	3605
Db	3295	CTGGTCTTACTCGAGACAGAAAGCTTTCCCGAGCCAAAGACCAGATTCACAGCCACTGGG	3354
OY	3606	CCCTTGATGTAGAGCTGGAGAGAGGCAATGCGAGAGGGGCCACCTCCGTTTCTCTG	3665
Db	3355	CCCATGTAGTGTAGAGCTGGAGAGAGGCACTGACAGAGGGGCCACCTCCATTGTCTG	3414
OY	3666	GAGACTAGACATAGATGGGATCTCGCTGATGTGAAGAACCTGGAGAACATCAGGAGCAAC	3725
Db	3415	GAGACAAAGCATAGATGGGATCTTCGCTGATGTGAAGAACTTGGAGAACATTAGGAGCAAC	3474
OY	3726	CTGGCCCCGGGCTGCTACAAATACCCAGGCTTTGAGCAACAGTGAAGCTGCTTAGAGAT	3785
Db	3475	CTGGCCCCAGGCTGCTACAAATACCCAGGCTTTGAGCAACAGTGAAGCTGCCATTAATAT	3534
OY	3786	TTTCTCAACCAAGGTTCTTGGATTCACAGCTACGCTGCTTGAAGATTTCTCA	3837
Db	3535	TTTCTCAACTGAGGTTCTTGGATTCACAGCTACGCTGCTGAGGAGCCATGTCA	3586

RESULT 11

ID AAT13324 standard; cDNA; 4316 BP.

AC AAT13324;

DT 13-NOV-1996 (first entry)

DE Kalinin/Iaminin 5 gamma-2 chain alternative coding sequence.

KW kalinin; lamolin; epidermolysis bullosa; junctional; probe;

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FT	CDS	118..3453
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FT /note= "kalinin/1aminin 5 gamma-2 chain"

PN WO9610646-A1

PD 11-APR-1996.

PF 04-OCT-1995; 95WO-EP03918.

PR 04-OCT-1994; 94US-0317450.

PA (TRYG/) TRYGGVASON K.

PI Kallunki P, Pyke C, Tryggvason K;

DR WPI; 1996-209366/21.

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PT detect, monitor and inhibit the invasive growth of cell in tissue

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a

3' end sequence from T13324, encoding the kalinin/laminin 5 gamma-2

CC from epidermolysis bullosa, esp. the junctional form (JEB). Probes and
CC antisense gamma-2 sequences derived from this sequence can be used to
detect, monitor and inhibit the invasive growth of cells in tissue,
CC partic. malignant tissue.

XX Sequence 4316 BP; 1158 A; 1033 C; 1226 G; 899 T; 0 other;

Query Match 68.3%; Score 2726; DB 17; Length 4316;
Best Local Similarity 88.5%; Pred. No. 0;
Matches 3045; Conservative 0; Mismatches 365; Indels 30; Gaps 7;

QY 99 AAGGAAAAAGAGGACACAGCGGAGCGGAGAGTGAAGTCCACGCGGCGAGCGCGGCG 158
Db 14 AAGGAAAAAGAGGACACAGCGGAGCGGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGT 158
QY 159 AGGAGACCCCTGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 211
Db 72 AGGAGACCCCTGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 131
QY 212 GCTGAGCTGCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 271
Db 132 GCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 191
QY 272 GGAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 331
Db 192 GGAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 251
QY 332 ACAGAGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 391
Db 252 ACAGAGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 311
QY 392 CGAGAGGTGACAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 451
Db 312 CGAGAGGTGACAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 371
QY 452 TTGTAATCTTAAGGTTCTCTTAAGGTTCTCTTAAGGTTCTCTTAAGGTTCTCTTAAG 511
Db 372 TTGTAATCTTAAGGTTCTCTTAAGGTTCTCTTAAGGTTCTCTTAAGGTTCTCTTAAG 431
QY 512 GCCAGGTGTGACAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 571
Db 432 ACCAGGTGTGACAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 491
QY 572 TGTGAGGTGCGCCAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 631
Db 492 TGTGAGGTGCGCCAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 551
QY 632 CATCTCAGGCGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 691
Db 552 CATCTCAGGCGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 611
QY 692 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 751
Db 612 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 671
QY 752 CCACTGTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 811
Db 672 CCACTGTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 731
QY 812 TAAATATATCT 871
Db 732 TAAATATATCT 791
QY 872 GTCTCCGCAAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 931
Db 792 GTCTCCGCAAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 851
QY 932 ATCAGACCCCTGTCT 991
Db 852 ACTAGATCTGTCT 911
QY 992 CGGCAAAAGCTTCT 1051

Db 912 TGGCAAAAGCCTGTCT 971
QY 1052 TGAAGTATCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1111
Db 972 TGAAGTATCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1031
QY 1112 GACACTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1171
Db 1032 GACACTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1091
QY 1172 TAAATGAGCCCCAGTAAATGATGATGATGATGATGATGATGATGATGATGATGATG 1231
Db 1092 TAAATGAGCCCCAGTAAATGATGATGATGATGATGATGATGATGATGATGATGATG 1151
QY 1232 CCGTCCGATCCGAGCTTCT 1291
Db 1152 CCGTCCGATCCGAGCTTCT 1211
QY 1292 GATTTGAGCCCGCTTCT 1351
Db 1212 GATTTGAGCCCGCTTCT 1271
QY 1352 TGTGAGTACAAAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 1411
Db 1272 TGTGAGTACAAAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 1331
QY 1412 CAGAGTGGAGCTTTGAGTACCTGATGATGATGATGATGATGATGATGATGATGATG 1471
Db 1332 GAGAGTGGAGCTTTGAGTACCTGATGATGATGATGATGATGATGATGATGATGATG 1391
QY 1472 TCCAGACACAGAGAGCTTACTCAGGAGATGAGAGATGAGAGATGAGAGATGAGAG 1531
Db 1392 TCCAGACACAGAGAGCTTACTCAGGAGATGAGAGATGAGAGATGAGAGATGAGAG 1448
QY 1532 CTGCCCCATGCTTCT 1591
Db 1449 CTGCCCCATGCTTCT 1508
QY 1592 TCCGAATGGGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1651
Db 1509 TCCGAATGGGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1568
QY 1652 CCCCAGGAGTACAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1711
Db 1569 CCCCAGGAGTACAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1628
QY 1712 CTTGCGGGAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1771
Db 1629 CTTGCGGGAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1688
QY 1772 CCGTATGAGCTTCT 1831
Db 1689 CCGTATGAGCTTCT 1748
QY 1832 CACAGCTGGGGTCCACTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1891
Db 1749 CACAGCTGGGGTCCACTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1808
QY 1892 CAATCCAGACAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1951
Db 1809 CAATCCAGACAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1868
QY 1952 GTGTGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 2011
Db 1869 GTGTGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1928
QY 2012 TGGCGACATGACAGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 2071
Db 1929 TGGAGCAAT---CAGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1985
QY 2072 TATGACAGAGTCCAGATCTCTGAGAGCCCTGATGATGATGATGATGATGATGATG 2125
Db 1986 TATGACAGAGTCCAGATCTCTGAGAGCCCTGATGATGATGATGATGATGATGATGATG 2045

QY 2126 AGTACCCAGACAGAGCTGGAGGCGAGAGATGACAGAGCTGAGAGGCCCTTGCGGACAT 2185
 DB 2046 AGTACCTGATACAGAGCTGGAGGCGAGAGATGACAGAGCTGAGAGGCCCTTGAGGACAT 2105
 QY 2186 TCTGAGAGAGAGCCCAAGTTTTCACAAAGTGTGTAGTCTCTCAATCTCCGGGTGCGCAA 2245
 DB 2106 TCTGAGAGATGCGCCAGTTTTCACAAAGTGTGTAGTCTCTCAATCTCCGGGTGCGCAA 2165
 QY 2246 GGCAGAGACTCAAGAGATAGTACCGGAGCCGCTGATGACCTCAAGATGACTGTGA 2305
 DB 2166 GGTGAGAGAGCCCAAGAGATAGTACCGGAGCCGCTGATGACCTCAAGATGACTGTGA 2225
 QY 2306 AAGAGTTGCGGCCCTTGCGGAGTCAATCAAGAACCAAGTTTCAGAGATCTGCGAGCTCAT 2365
 DB 2226 AAGAGTTGCGGCCCTTGCGGAGTCAATCAAGAACCAAGTTTCAGAGATCTGCGAGCTCAT 2285
 QY 2366 CACTGAGTGGGCTGAGAGCTGAGAGAAATGAGGCTTCCCTGCAAAACCAACATCTCC 2425
 DB 2286 CACTGAGATGACACTGAGCTGAGAGAAATGAGGCTTCCCTGCAAAACCAACATCTCC 2345
 QY 2426 TCCCTGAGACACTAGCTGAGGCGCAATGCTTTAAAGTCTGAGTCAAGAGGCGACAG 2485
 DB 2346 TCGCTGAGACACTAGCTGAGGCGCAATGCTTTAAAGTCTGAGTCAAGAGGCGACAG 2405
 QY 2486 ATTGGCAGACAGCCATGTTTCACTAGCCAGTAAACATGAGACAACTGCGAAAGAAACCA 2545
 DB 2406 ATTAGCAGAAAGCCAGCTGAGTCAAGTCAACATGAGACAACTGCAAGAGGAACTGA 2465
 QY 2546 GAGAGTATCCAAAGAGCTGATGTCACCTGCTGCGCGAGGCTCTGAGAGAGAG- - - - -G 2599
 DB 2466 GAGCTATTCCTCAAAAGCCCTCTACCTGCTGCGCGAGGCGCTCTGAGAGAGCTGCGAG 2525
 QY 2600 CGGAGGCGGAGCTGAGGCGAGGCGGCTGCTGCAAAAGCTTGTGGAAATTTGCAAGAAAC 2659
 DB 2526 CGGAGGCGGAGCTGAGGCGAGGCGGCTGCTGCAAAAGCTTGTGGAAATTTGCAAGAAAC 2585
 QY 2660 TAAATCTCTGCGCCAGAGATGTCGAGGAGGCCAGCAACGACATGAGAGAGATAG 2719
 DB 2586 CAGTCCCTGCGCGAGAGTGTGACAAAGGAGCGCACCAAGCGGAAATTTGAAACAGATAG 2645
 QY 2720 GTCTTATCAGCATAGTCTCCAGCTTCCATTCCTGCTGCTCAATTCAGGAGGATCATGA 2779
 DB 2646 GTCTTATCAGCATAGTCTCCAGCTTCCATTCCTGCTGCTCAATTCAGGAGGATCATGA 2705
 QY 2780 TCACTCCCTGAGGT- - -AGAGCGAGAGAGCTCAGACCAAAAGAGTCTCTCTCAAA 2836
 DB 2706 TCACTCCCTGAGGTGAGAGAGAGAGAGATCAAAAGAGCGGATTCACCTCTCAAG 2765
 QY 2837 CCGTGTGACTTAACATATGATGATGATCAAGCAGCTGCAAAAGCAATCTGGGAAACTGGGA 2896
 DB 2766 CCGTGTGAAACAGGATATGATGATGATCAAGCAGCTGCAAAAGCAATCTGGGAAACTGGGA 2825
 QY 2897 AGAAGAAACCCGAGAGCTTTACAGATGAGAAAGATGAGAGACAGATCATCATGAGCT 2956
 DB 2826 AGAAGAAACCCGAGAGCTTTACAGATGAGAAAGATGAGAGAGAGATCATCATGAGCT 2885
 QY 2957 GCTTTCCCGTGCACACTTGTCTTAAAGCAGAGCCCAAGAGCACTAAGTATGGGCAATGC 3016
 DB 2886 GCTTTCCCGTGCACACTTGTCTTAAAGCAGAGCCCAAGAGCACTAAGTATGGGCAATGC 2945
 QY 3017 CACTTTTATGAAGTTGAGACATCTTAAAGATCTCAGAGAGTTGACCTGCAAGTTGG 3076
 DB 2946 CACTTTTATGAAGTTGAGACATCTTAAAGATCTCAGAGAGTTGACCTGCAAGTTGG 3005
 QY 3077 AGATAAAGAGCGAGAGCTGAAGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 3136
 DB 3006 CAAACAGAAAGCGAGAGCTGAAGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 3065
 QY 3137 TGCAGGTGCGAGTGAAGT 3196
 DB 3066 TTCAGATGCCAGTGAAGT 3125

QY 3197 CGCCCAAGAGGCGCAAGAGATGACAGGAGAGGCGCTGAGAGATCTTGGCAAGATAGAACCA 3256
 DB 3126 TGCACAGAGAGGCGCAAGAGATGAGGCGGAGGCGCTGGAATCTCCAGTGAATGACCA 3185
 QY 3257 GAGATGAGAGAGTCTGAGACTTGGAGGCAATGAGAGAGAGAGAGAGAGAGAGAGAGAG 3316
 DB 3186 GAGATGAGAGAGTCTGAGACTTGGAGGCAATGAGAGAGAGAGAGAGAGAGAGAGAGAG 3245
 QY 3317 GAGGAGAGGCGCACTGAG 3376
 DB 3246 AAGGAGAGGCGCTGCTGAG 3305
 QY 3377 GAGAGAGAGAGTGTGACATGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3436
 DB 3306 GAGAGTGAAGTGTGACAGAGATGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 3365
 QY 3437 AGTTGAAAGAGAGGCGCAAG 3496
 DB 3366 GGTGATGATGAG 3425
 QY 3497 TGGCATCTGACACTTAATAG 3516
 DB 3426 CGGCTCTGCTGATCTGATGG 3445
 RESULT 12
 AAL42911
 ID AAL42911 standard; cdna; 4316 BP.
 XX
 AC AAL42911:
 XX
 DT 05-AUG-2002 (first entry)
 XX
 DE Laminin gamma-2 chain cdna sequence 2.
 XX
 KW Laminin gamma-2; gene; ss; cancer; laminin gamma-2 chain inhibition;
 KW carcinogen inhibition; anti-gamma-2 chain antibody;
 KW epithelial cell adhesion; laminin-5.
 XX
 OS Unidentified.
 XX
 FH Key location/Qualifiers
 FT 118..3453
 FT CDS
 FT
 FT sig_peptide /product= "Laminin gamma-2 chain 2"
 FT 118..183
 FT mat_peptide /*tag= b
 FT 184..3450
 FT /*tag= c
 FT /note= "Mature laminin gamma-2 chain 2"
 PN US2002052307-A1.
 PD 02-MAY-2002.
 PE 08-JAN-2001; 2001US-0756071.
 XX
 PR 07-JAN-2000; 2000US-175005P.
 PR 04-OCT-1994; 94US-0317450.
 PR 18-FEB-1997; 97US-0800593.
 PR 15-SEP-2000; 2000US-0663147.
 PA (TRYG/) TRYGVASON K.
 PA (KALU/) KALUNKI P.
 PA (PYKE/) PYKE C.
 XX
 PI Trygvason K, Kallunki P, Pyke C;
 DR WPI; 2002-434824/46.
 DR P-PDB; AAO14993.
 XX
 PT Modulating laminin 5 gamma 2 chain interactions of invasive carcinogens
 PT for treating cancers and promoting attachment of cultured cells in

PT vitro -
XX
PS Example 1: Page 26-30; 51bp; English.
XX

CC The invention comprises a method of inhibiting the laminin gamma-2 chain
CC interactions of invasive carcinogens with surrounding tissues - by using
CC anti-gamma-2 chain antibodies to inhibit the gamma-2 chain biological
CC activity of the invasive carcinogens. The invention also comprises a
CC method for promoting adhesion of epithelial cells by exposing the cells
CC to intact laminin-5 molecules. The first method of the invention is
CC useful for preventing gamma 2 chain interactions of invasive carcinogens
CC with surrounding tissues. The second method of the invention is useful
CC for promoting adhesion of cultured epithelial cells. The present CDNA
CC sequence encodes a laminin gamma-2 chain.
CC
XX
SQ Sequence 4316 bp; 1158 A; 1033 C; 1226 G; 899 T; 0 other;

Query Match 68.3%; Score 2726; DB 24; Length 4316;
Best Local Similarity 88.5%; Pred. No. 0;
Matches 3045; Conservative 0; Mismatches 365; Indels 30; Gaps 7;

OY 99 AAGGAAAGGAGGACACAGCGGAGCGAGTGAAGTCCCGAGCGGCGGCGCGGCG 158
DB 14 AAGGAAAGGAGGACACAGCGGAGCGAGTGAAGTGAAGTGAAGTGAAGTGAAGT 71
OY 159 AGGACCCCTGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 211
DB 72 AGGACCCCTGACGCGGAGACAGAGACTGAAGCGGCGGCGGCGGCGGCGGCGGCGGCG 131
OY 212 GCTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 271
DB 132 GCTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 191
OY 272 GGAAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 331
DB 192 GGAAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 251
OY 332 ACAGACAGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 391
DB 252 ACAGACAGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 311
OY 392 CGAAGTGTGACAGGAGGATTTACCGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 451
DB 312 CGAAGTGTGACAGGAGGATTTACCGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 371
OY 452 TTGTAAGTCTAAGGATGCTTGAAGGCTGATGATGATGATGATGATGATGATGATGAT 511
DB 372 TTGTAAGTCTAAGGATGCTTGAAGGCTGATGATGATGATGATGATGATGATGATGAT 431
OY 512 GCCAGTGTGACAGGAG 571
DB 432 ACCAGTGTGACAGGAG 491
OY 572 TGTGAGTGTGCGCCAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 631
DB 492 TGTGAGTGTGCGCCAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 551
OY 632 CATCTCAGAGGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 691
DB 552 CATCTCAGAGGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 611
OY 692 CTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 751
DB 612 CTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 671
OY 752 CCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 811
DB 672 CCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 731
OY 812 TAAATATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 871
DB 732 TAAATATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 791

OY 872 GTCTCTGCAAGAGCTCCAGTGTACACAGCGCATCGGATATATATATATATATATATAT 931
DB 792 GTCTCTGCAAGAGCTCCAGTGTACACAGCGCATCGGATATATATATATATATATATAT 851
OY 932 ATCAGACCCCTGCTATTTTGTAGTCTGCGCAAAATTTTGTGGAAATCAACAGGTAGCTA 991
DB 852 ACTGATGATCTGCTATTTTGTAGTCTGCGCAAAATTTTGTGGAAATCAACAGGTAGCTA 911
OY 992 CGGGAAAGCGCTATCTTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1051
DB 912 TGGGAAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 971
OY 1052 TGAGTGTATCTGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1111
DB 972 TGATGTATCTGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1031
OY 1112 GACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1171
DB 1032 GACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1091
OY 1172 TAAATGAGCGCGGCAAGTAAATTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1231
DB 1092 TAAATGAGCGCGGCAAGTAAATTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1151
OY 1232 CCTGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1291
DB 1152 CCTGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1211
OY 1292 GATTTGACCGCGCGGCTTGTGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1351
DB 1212 GATTTGACCGCGCGGCTTGTGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1271
OY 1352 TGTGAGTGTGAG 1411
DB 1272 TGTGAGTGTGAG 1331
OY 1412 CAGACTGAG 1471
DB 1332 GAGACTGAG 1391
OY 1472 TCAGACACAG 1531
DB 1392 TCAGACACAG 1448
OY 1532 CTGCGGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1591
DB 1449 CTGCGGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1508
OY 1592 TCGCAATGAGTGTGAG 1651
DB 1509 TCGCAATGAGTGTGAG 1568
OY 1652 CCCCCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1711
DB 1569 CCCCCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1628
OY 1712 CTTGCGGAG 1771
DB 1639 CTTGCGGAG 1688
OY 1772 CCTGATGAGTGTGAG 1831
DB 1689 CCTGATGAGTGTGAG 1748
OY 1832 CACAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1891
DB 1749 CACAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1808
OY 1892 CAATCCAGACAG 1951
DB 1809 CAATCCAGACAG 1868
OY 1952 GTGTGAG 2011

1869 ATTCGAAAGTGAAGGACCTGTGTCGCAAGCAGGATTTGGGCCCCAACGTGCGCA 1928
 2012 TGGGCACTGACGAGTGTCCAGCTTGTCTAATCAAGTGAAGTTTCAGATGATGATGAT 2071
 1929 TGGAGCATTT---CAGCTGTCCAGCTTGTCTAATCAAGTGAAGTTTCAGATGATGATGAT 1985
 2072 TATGACAGCAGCTCCAGATCTGAGAGCCCTGATTTGCAAGGCTCAGG---TGGAGC 2125
 1986 TATGACAGCAGCTCCAGATGAGAGGCTGATTTTCAAGGCTCAGGAGGCTGATGAGT 2045
 2126 AGTACCAAGCAGCAGAGCTGGAAGGAGATGACAGCAGGCTGACAGGCTTGGGAGCAT 2185
 2046 AGTACCTGATACAGAGCTGGAAGGAGATGACAGCAGGCTGACAGGCTTGGGAGCAT 2105
 2186 TCTGAGAGAGCCAGATTTCAAGAGTGTGTTAGATCTTCAATCTCCGGGTGGCCAA 2245
 2106 TCTGAGAGAGTCCCAAGTTTCAAGAGTGTGTTAGATCTTCAATCTCCGGGTGGCCAA 2165
 2246 GGCAGAGACTCAAGAGATAGTACCGGGAGCCGCTGATGATGACCTCAAGATGATGATGA 2305
 2166 GGTGAGAGAGCCCAAGAGATAGTACCGGGAGCCGCTGATGATGACCTCAAGATGATGATGA 2225
 2306 AAGAGTTCCGGGCTGAGGAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 2265
 2226 AAGAGTTCCGGGCTGAGGAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 2285
 2366 CACTCAGATGACAGCTGAGGCTGAGGAGTATGATGATGATGATGATGATGATGATGATGAT 2425
 2286 CACTCAGATGACAGCTGAGGCTGAGGAGTATGATGATGATGATGATGATGATGATGATGAT 2345
 2426 TCCCTCAGAGCAGTACGTGGGAGGAGTATGATGATGATGATGATGATGATGATGATGATGAT 2485
 2346 TGCCTCAGAGCAGTACGTGGGAGGAGTATGATGATGATGATGATGATGATGATGATGATGAT 2405
 2486 ATTGGCAGAGCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2545
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 2546 GGAATATTTCCAAAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2599
 2466 GGAATATTTCCAAAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2525
 2600 CGGAGGAGGAGCCTGAGAGGAGCCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2659
 2526 CGGAGGAGGAGCCTGAGAGGAGCCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2585
 2660 TAAATCTGTGGCCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2719
 2586 CAAATCTGTGGCCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2645
 2720 GTCTTATCAAGATAGTCTCCAGCTTCTCAATTCGATGATGATGATGATGATGATGATGATGATGAT 2779
 2646 GTCTTATCAAGATAGTCTCCAGCTTCTCAATTCGATGATGATGATGATGATGATGATGATGATGAT 2705
 2780 TCAATCTGTGGCCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2836
 2706 TCAATCTGTGGCCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2765
 2837 CCGTGTGATCAAGATAGTCTCCAGCTTCTCAATTCGATGATGATGATGATGATGATGATGATGATGAT 2896
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 2897 AGAAGAAACCCGAGCTCTTACAGATGGAAGAAATGAGAGACAGATCAGATCAGCT 2956
 2826 AGAAGAAACCCGAGCTCTTACAGATGGAAGAAATGAGAGACAGATCAGATCAGCT 2885
 2957 GCTTCCCGTGGCAACTGTCTAAGAGAGCCCAAGAGACAGATCAGATCAGCT 3016
 2886 GCTTCCCGTGGCAACTGTCTAAGAGAGCCCAAGAGACAGATCAGATCAGCT 2945
 3017 CACTTTTATGAAGTGAAGACATCTTAAAGATTCAGAGAGTTGACCTGACGTTGG 3076

2946 CACTTTTATGAAGTGAAGACATCTTAAAAACCTCAGAGAGTTGACCTGAGGTTGA 3005
 3077 AGATTAAGAGAGAGAGCTGAAGAGGAGATGAGAGAGCTCTCTACATCAGCAGAGAT 3136
 3006 CAACAGAAAGAGAGAGCTGAAGAGGAGATGAGAGAGCTCTCTACATCAGCAGAGAT 3065
 3137 TGCAGGTGAGAGAGAGCTGAAGAGGAGATGAGAGAGCTCTCTACATCAGCAGAGAT 3196
 3066 TGCAGGTGAGAGAGAGCTGAAGAGGAGATGAGAGAGCTCTCTACATCAGCAGAGAT 3125
 3197 CGGCAAGAGAGAGAGCTGAAGAGGAGATGAGAGAGCTCTCTACATCAGCAGAGAT 3256
 3126 TGCAGAGAGAGAGAGCTGAAGAGGAGATGAGAGAGCTCTCTACATCAGCAGAGAT 3185
 3257 GGAATAGAGAGAGCTGAAGAGGAGATGAGAGAGCTCTCTACATCAGCAGAGAT 3316
 3186 GGAATAGAGAGAGCTGAAGAGGAGATGAGAGAGCTCTCTACATCAGCAGAGAT 3245
 3317 GAAGGAGCTGAGAGCTGAAGAGGAGATGAGAGAGCTCTCTACATCAGCAGAGAT 3376
 3246 AAGAGAGCTGAGAGCTGAAGAGGAGATGAGAGAGCTCTCTACATCAGCAGAGAT 3305
 3377 GGAAGAGAGAGAGCTGAAGAGGAGATGAGAGAGCTCTCTACATCAGCAGAGAT 3436
 3306 GGAAGAGAGAGAGCTGAAGAGGAGATGAGAGAGCTCTCTACATCAGCAGAGAT 3365
 3437 AGTTGAAGAGAGAGCTGAAGAGGAGATGAGAGAGCTCTCTACATCAGCAGAGAT 3496
 3366 GGTGATACAGAGAGCTGAAGAGGAGATGAGAGAGCTCTCTACATCAGCAGAGAT 3425
 3497 TGGATCTCTACAGCTTAATAG 3516
 3426 CGGCTCTCTACAGCTTAATAG 3445

RESULT 13
 AAC83733
 ID AAC83733 standard; cdna; 5159 BP.
 XX
 AAC83733;
 XX
 02-MAR-2001 (first entry)
 DT
 XX
 DE Mouse laminin 5 cdna, SEQ ID NO: 33.
 XX
 KW Mouse; laminin 5; vulnery; antilucer; antiinflammatory; antidiabetic;
 KW cell adhesion promoter; wound healing; ulcers; burn; skin graft;
 KW periodontitis; gingivitis; Type I diabetes; angiogenesis regulation; ss.
 XX
 OS Mus musculus.
 XX
 WO200066731-A2.
 PN
 PD 09-NOV-2000.
 XX
 PF 28-APR-2000; 2000MO-US11459.
 XX
 PR 30-APR-1999; 99US-0131720.
 PR 21-AUG-1999; 99US-0149738.
 PR 24-SEP-1999; 99US-0155945.
 XX
 PA (BIOS-) BIOSPARTUM INC.
 XX
 PI Boutaud A;
 XX
 DR WPI; 2000-687538/67.
 DR P-PSDB; AAB48472.
 XX
 PT Laminin 5-expressing cells, used to accelerate wound healing associated
 PT with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
 PT burns, acute wounds and skin grafts -
 XX
 PS Claim 4; Page 213-219; 232pp; English.

OY	2103	ATTTCGAAAGGCTCAGGGGTGGAGACGATACCCAAACCAG-----ACGTGGAAAGCCAGG	2153
Db	1945	GTTCCTAAAGGGCTCAGGGGTGGGTGGTGGTGTGCTACAGTCCCAAGTGCACGTCTGGAAAGGCG	2004
OY	2154	ATGCAGCAGGCTGGAGCAGAGCCCTTCGGGACATTCCTGGAGAGAAAGCCAGATTTTCACAAGAT	2213
Db	2005	ATCGAGCAGGCTGAGCAGAGCCCTTCAGGACATTCCTGGAGAAAGCTCAGATTTTCAGAAAGG	2064
OY	2214	GCTGTAGATCCTTCATCTCCGGGTGGCCCAAGGCAMGAGCTCAGAGAAATAGTACCGG	2273
Db	2065	GCAATGAAAGCCGTGTCTGTCCGGCTGGCCCAAGGCACAGGAGCACAAGAAAGCACTACAAG	2124
OY	2274	GACCGCCCTGGATGACCTCAGATGACGTGGAAAGAGTGGGGCCCTGGGAGTCAGAT	2333
Db	2125	ACCGCCCTGGATGACCTCAGATGACGTGGAAAGAGTGGGGCCCTGGGAGTCAGAT	2184
OY	2334	CAGAAACCAAGTTCAGAGTACTCGCAGAGGCTCATCTACAGATGGCCCTGAGGCTTGAGAA	2393
Db	2185	CAGAAACCAAGTTCAGAGTACTCGCAGAGGCTCATCTACAGATGGCCCTGAGGCTTGAGAA	2244
OY	2394	AGTGAAGCTTCCCTGCAAAACCAACACTTCTCCTTCAGAGCACTACGTGGGCCAAT	2453
Db	2245	AGCGAAGCTCCTTGGAAAAACCTAATATCCATTCTTCTGAGCACTACGTGGGCCAAT	2304
OY	2454	GGCTTTTAAAGTCGGGCTCAGAGGCCACGAGATTTGGAGACACCCAAAGTTCAGTACGCC	2513
Db	2305	GATTTTAAAGTCGGGCTCAGAGGCCACGAGATTTGGAGACACCCAAAGTTCAGTACGCC	2364
OY	2514	AGTAACATGAGCACTGGCCAAAGGAAACCAGGAGTATTCCAAAGAGCTGATGTCACTG	2573
Db	2365	AAGCAATGAGCACTGGCCAAAGGAAACCAGGAGTATTCCAAAGAGCTGATGTCACTG	2424
OY	2574	GTGGCCAGGCTCTGCAAGAAAGAGGCGGAAAGCCGACCTGACACGAGCCGTGTGCAG	2633
Db	2425	GCCGCGCAAGCTTGTGAGTGGAGAGGCGGAAAGTGGCTTGGGACAGCTCCGTGTACAA	2484
OY	2634	AGGCTTGGGAAAAATTGCAGAAAACTAAATCTGTGGCCCAAGGATTCGAGGAGAGGCC	2693
Db	2485	GCTCTTAGGAAAAATTGAGAAAAACCAAGTCCCTGAGCCAGCAGCTGTCACTTGGAGGCC	2544
OY	2694	ACGCAAAACGACATGGAAGCAGATAGTCTTATCAGCATAGCTTCACACTTCCTCAATTCC	2753
Db	2545	ACCCAAAGCCGACATTTGAAGTGAAGGCGTATCAGCACATCTCCGCTCTCGATTCT	2604
OY	2754	GTCGTCGATTCACGGGATCAATGATCAGTCCTTGACGCTAGAAAGGAGAGGCTCAGA	2813
Db	2605	GCCTCTCAGCTTCAGGGAATCAGATATCTGCTTTAGGTGGAAGCAAAAGGATCAGA	2664
OY	2814	CAAAAAGCTGATTCCTCTCAAAACCGTGTGACTAAGCATATGATGATTCAAACACGTG	2873
Db	2665	CAAAAAGCTGATTCCTCTCAAAACCGTGTGACTAAGCATATGATGATTCAAACACGTG	2724
OY	2874	CAAAAGCAATCTGGGAAACTGGGAAAGAAACCAGGACGCTTTACAGAAATGAAAGAT	2933
Db	2725	CGAAACCAATCTGGGAAACTGGGAAAGAAACCAGGACGCTTTTACAGAAATGAAAGAT	2784
OY	2934	GGGAGACGACATCAGATCAGCTGCTTCCCGTCCCAACCTTGCTAAAGGAGAGCCCA	2993
Db	2785	AGGAGACGACATCAGATCAGCTGCTTCCCGTCCCAACCTTGCTAAAGGAGAGCCCA	2844
OY	2994	GAAGCACTAATGATGGCAATGCCACTTTTATAGTTAGATTGAACATCTTAAAGAAATCTC	3053
Db	2845	GAAGCGGTAAATGATGGGAATGCCACTTTTATAGATTGAACATCTTGAAGAAACTCTC	2904
OY	3054	AGAGCAATTTGACCTGCAAGTTTGGAGATPAAAAGACAGAGAGCTGAAGAGCCATGAAGA	3113
Db	2905	CGAAGATTTTGTCTGCAAGTTTGGAGACAGAAAACAGAGGCTGAAGAGCCATGAAGA	2964
OY	3114	CTCTCCATCATCAGCCAGAAAGTTGGAGGTGCCAGTGCACAGAGCAAGCAAGCAAGCA	3173
Db	2965	CTCTCCCTTATTTAACCAGAAAGTTGGCGATGCCAGTGCACAGAGCAAGCAAGCAAGC	3024

OY		3174	GCCCCGGGACAGTGCCTGCCCGCAGCCGCCAAGAGGGCAAAAGAATTCGAAGCCAGGAGGCCCTG	3233
OY		3175	GGCCCTGGGAGAGGCGCACTGCTCCGACACCACAAGGGCAAGAAGCCAGCTAGGGAAGGCTTG	3084
Db		3025	GCCCTGGGAGAGGCCACTGCTCCGACACCACAAGGGCAAGAAGCCAGCTAGGGAAGGCTTG	3084
OY		3234	GAGATCTCTGGCAAGATATGAACACAGAGAGATAGAGAGTGTGAATTGGAAGCCAAATGTGACA	32933
Db		3085	GAGATCACACACAGAGATAGAGCTGTGAGATATAGAGATGTGAATCTTTGAAGCTTAATGTGACA	3144
OY		3234	GCAGATGAGGCGCTTGGCCCATGGAAAAGGAGCTCCCACTCTGGAAGAGCGAGATATGAGAG	3204
Db		3145	GCAGATGAGGCGCTTGGCCCATGGAAAAGGAGCTCCCACTCTGGAAGAGCGAGATATGAGAG	3204
OY		3354	GTGGAGSAGAGAGCTGTCAAGGAGAGAGAGTAGTTTGACATGATGATGAGAGCGAGTGCAG	3413
Db		3205	ATG--ATTGAGCTGTGGCCAGAAAGGAGCTGGAGTTTGACACAGGATTAAGACACGCTCCAG	3261
OY		3414	ATGCTAATTGTGAGAGGCGCCCAAAGATGTGAAAAACAGAGCCAAGATGCTGTGAGTTACGATC	3473
Db		3262	CTGTGTGATTACTGAAAGCCCAACAGCTGTATGCCAGAGACAGAGACTGCCGGAGTTACCATC	3321
OY		3474	CAAGACACACTCAACACACTTGTGATGGCATCTTACACCTAATATAGACACAGCTGGCAGTGTG	3533
Db		3322	CAAGACACRCTCAACACACTTGTGAGCGGCATCTTACACCTCAATAGACACAGCTGGCAGTGTG	3381
OY		3534	GATGAAGAGAGAGCTGTATCTACTGAGCAGAGAAGCTTTCCAGACCAAGACTCAAGATCAAC	3593
Db		3382	GATGAAGAGAGAGATGTATGATCTATTGAAACAAAGGCGTTTTCCAAAGCCAAAGCCAAATCAAC	3441
OY		3594	AGCCACGCTAGAGGCCCTTGATGTCAAGAGCTGGAAGAGAGGCGCACATCGGCAAGAAAGGCCAC	3653
Db		3442	AGTGCACCTTGGGCCCCCTTGATGTCTGACCTTGGAGAGAGAGGCTGCTCGGCAAGAACCCAC	3501
OY		3654	CTCCGTTTCTGAGAGACTAGCATAGATGGATCTGTGCTGATGTGAAAGAACTTGGAGAAC	3713
Db		3502	CTCCATCTGCTGGAAGACTAGCATAGATGGATCTTGTGTGATGTGAAGAACCTGTGAGAAC	3561
OY		3714	ATCAGGGACAACCTGCCCCGGGCTGCTACAAATCCAGAGCTCTTGAGACAAGTGAAC	3773
Db		3562	ATTGAGAGCAACCTGCCCCAGGCTGTCTACAAATCCAGAGCTCTTGAGACAACGTTGAAGT	3621
OY		3774	TGCCCTAGAGATTCTCTCAAC	3793
Db		3622	TGTCAATAGAGATTGTCTCAC	3641
<hr/>				
RESULT 14				
ADB31144				
ID	ADB31144	standard;	cdna:	3579 BP.
XX	ADB31144;			
AC				
XX				
XX	21-AUG-2002	(first entry)		
XX				
DE	Mouse laminin gamma2 chain cdna.			
XX				
KW	Cancer; cell proliferation; integrin receptor; signalling pathway;			
XX	gene therapy; mouse; laminin gamma2; ss.			
OS	Mus sp.			
XX				
FH	Key	Location/Qualifiers		
FT	CDS	1..3579		
FT		/tag= a		
XX		/product= "Laminin gamma2 chain"		
FN	WO200230465-A2.			
XX				
PD	18-APR-2002.			
XX				
PF	12-OCT-2001; 2001WO-US32127.			
XX				
PR	12-OCT-2000; 2000US-239705P.			
PR	24-OCT-2000; 2000US-242812P.			

OY	1935	GGCTGCGAGCCCTGTGAGTGTGCGAAGTGTATGGCACTGTGTTTGGCAACCGAGGCTTGGT	199
Db	1738	GGTGGGAGCCCTGGAGAGTGTTCGAGGTATGGCACTGTGTTTGGCAACCGAGGCTTGGC	1799
OY	1995	GGCTCAGCTGTGAGCATTCGGGCACTGCACGACTGTCCAGCTTGTATATCAAGTGAAG	2054
Db	1798	GGCTTCACTGTGATCAGCAGACCCCTTAACAGTTGTCTCGTGTACTAATCAAGTGAAG	1857
OY	2055	GTTCAAGATGANTCAATTTATGACAGAGTCCAGATCCTTGGAGGCGCTTATTTCCAGAGCT	2114
Db	1858	ATTCAAGATGACCACTTTTACCCAGAGTCCAGAGCTTGGAGGCGCTTGTTCAAAGGCT	1917
OY	2115	CAGGCTGGAGCAGT-----ACCAACCGAGAGCTGGAAGCGCAGATCAGCAGGCT	2165
Db	1918	CAGGCTGGAGGAGTGAGTGTGATCAAGTCCAGTGCAGTGGAAAGCAGGATGAGCAGGCT	1977
OY	2166	GAGCAGGCGCTTCGGGACATTCGAGAGAACCCAGATTTCAACAATGCTTTAGATCC	2225
Db	1978	GAGCAGGCGCTTCAGGACATTCGAGAGAACCTCAGATTTCAAGAGGGCAGATGAGGCC	2037
OY	2226	TTCAATCTCCGGGTGGCCAAAGCAAGCACTAAGAGAAATAGCTATACCGGAGCGGCTGGAT	2288
Db	2038	GTTGCTGTCTCCGGCTGGCCAAAGCAAGAGCCAAAGAACACTACAAACCCGCTGGAT	2097
OY	2286	GACCTCAAGATGACTGTGGAAGAGTTCGGGCGCTGGGCACTAGTATCAGAACCAAGTT	2345
Db	2098	GACCTCAAGATGACTGCAGAAAGAGTCCGGGCGCTGGGCACTAGCATCAACACAGAGTT	2157
OY	2346	CAGGATCTCGAGGCTCATCACTACAGATGGGCGGCACTGAGGAGGAAGAGAGGCTCC	2405
Db	2158	CAGGATCTCGAGGCACTCATCTCAGATGGGCGGCACTGAGGAGGAAGAGGCTCTC	2217
OY	2406	CTGCAAAACACCAATTCCTCTTCAAGCACTACGTGGGCGCAAAAGGCTTTAAAGT	2465
Db	2218	TTGGAACACACTAATATCATTTCTTCTGAGCACTACGTTGGGCGGAATGATTTAAAGT	2277
OY	2466	CTGGCTCAGGAGGCCACAGATTTGGCAACACCATGTTCACTAGCCAGTAACATGCA	2525
Db	2278	CTGGCTCAGGAGGCTCAAGAAAGGCAACACCGCTGAGTCAAGCTAACGCAATGCA	2337
OY	2526	CACCTGGCAAGAAACCCAGAGATTTCCAAAGAGCTGATGCTGCTGGCGAGAGCT	2585
Db	2338	CAACTGCAAGGAAACCTGAGAGACTACCTCAAAACAGCACTTCACTTGGCCCGCAAGCTC	2397
OY	2586	CTGCAGAGAAAGCGCGGAAGCGGCACTGAGCGAGCGCTGGTGTGCAAAAGCTTGTGGGA	2645
Db	2398	TTGAGTGGAGAGGCGGAAGTGGCTTGGAGACACTCCGTGTGTACAAAGGCTTTATGGGA	2457
OY	2646	AAATGTGCGAAAACTTAATCTCTGGCCCCAGGAGTTGTGAGGAGAGGCGCACCAACGAC	2705
Db	2458	AAATTAGAAGAAACCAAGTCCCTGAGCCAGCAGAGCTGTATTGGAGGCAACCCAGCGAC	2517
OY	2706	ATGGAAGCAGATAGGCTTTATCAGCATAGTCTCCACCTTTCATATTCGCTGTCAAGTT	2765
Db	2518	ATTGGAAGCTATAGTCTGTATCAGACAGTCTCCGCGCTCTGAGATTCTGCCTCTCAGCTT	2577
OY	2766	CAGGAGTCATAGATCAGTCCCTTGGAGGTAAAGGGAAGAGGCTCAGCAAAAAGCTGAT	2825
Db	2578	CAGGAGTCAGTGTCTCTCTTCAGGTGGAAGGAAGAGGATTCAGCAAAAAGGCTGAT	2637
OY	2826	TCTCTCTCAAAACCGTGTACTAGCATATGAGATGAGTTCAAGCAGCTGCAAGCAATCTG	2885
Db	2638	TCTCTCTCAAAACCGTGTGTACAGCAAAAGGATGATTCAGCGGTGTGCAAAACATCTG	2697
OY	2886	GGAACCTGTGGGAAGAAACCCGCGAGCTTTACAGAAATGGAAGATGGAGACAGACA	2945
Db	2698	GGAACCTGTGGGAAGAAACCGCGAGCTTTTACAGACTGGAAGAGATGAGAGACAGACT	2757
OY	2946	TCAGATCAGCTGTTCCTCCGTCGCAACCTTCTTAAAGCAGAGCCAAAGAGCACTAAGT	3005
Db	2758	TCAGATCAGCTGTTCCTCCGTCGCAACCTTCTTAAACAGAGCCAAAGAGCGCTAAGT	2817
OY	3006	ATGGGCAATGCCACTTTTATGAAGTTGAGAACACTTAAAGAAATCTCAGAGATTTGAC	3065

Db	2818	ATGGGCATATGCCACTTTTATGAAGTTGAGAACATCTCTGAAGAACCTCCGAGATTGAT	2877
Qy	3066	CTGCAGGTTGGAGATTAAGAAGCAGAAAGCTGAAGAGGCCATGAAGAGACTCTCTACATC	3125
Db	2878	CTGCAGGTTGAAGACAGAAAGCAGAGAGCTGAAGAGGCCATGAAGAGACTCTCTATTT	2937
Qy	3126	AGCCAGAAAGGTTGCAGGTGCCAGTACAAAGCAAGCAAGCAAGAAAGAGAGCCCGGAGT	3185
Db	2938	AGCCAGAAAGGTTGGAGATTCAGTACAAAGCCAGCAAGCAAGCAAGAAAGAGCCCTGGGAGC	2997
Qy	3186	GCTCTGCGCAGCGCCAGAGGGCAGAAAGATTCACACCAGAGAGGCCCTCGAGATCTCTGC	3245
Db	2998	GCCACTGCGCAGACCAGCAAGCGGCAAGAGCAGCTTAGGGAGGCCCTGGAGATCAGCAGC	3057
Qy	3246	AAGATTAAGCAAGGAGATATGAGAGTCTGACCTTGGAAAGCAATGTGAACAGATGAGACC	3305
Db	3058	GAGATTAAGGCTGGAGATATGAGAGTCTGAACTTGGAACTAATGTGACAGAGATGGGGCC	3117
Qy	3306	TTGGCCATGAGAGAGGCACTGGCCACTCTGAAAAGTGAATGAGAGAAAGTGGAAAGAGAG	3365
Db	3118	TTGGCCATGAGAGAAAGGCACTGCCACCTCTGAAGAGCAGATGAGAGAGATG ---ATTGAG	3174
Qy	3366	CTGTCAAGGAAGAGAGAGAGCTTTGACATGGATATGACGCGATGACAGATGTTAATGCA	3425
Db	3175	CTGGCCAGAAAGAGAGCTGGAGTTGACACGGATTAAGACACAGGTGACAGCTGTGATTA	3234
Qy	3426	GAGGCCCAAGAGATGTAACACAGAGCCAGAAAGTCTGAGTACGATCCAGAACACACTC	3485
Db	3235	GAAAGCCAGCAAGCTGATGCCAGAGCCAGAGTCCGGAGTTACATCCAAAGACACACTC	3294
Qy	3486	AACACATTTGATGAGCATCTTACACCTTAATAGACACAGCCTGGCAGTGTGATGAAGAGAG	3545
Db	3295	AACACATTTGAGCGGCATCTTACACCTTAATAGACACAGCCTGGCAGTGTGATGAAGAGAG	3354
Qy	3546	CTGATCTTACCTGGAGAGAGAGCTTTTCCGAGCCAGAGCTCAGATCAACAGCCAGCTACGG	3605
Db	3355	ATGATGCTATTATTAAGCAAGGGCTTTTCCAAAGCCAGAGCCAGATCAACAGCTGACCTGG	3414
Qy	3606	CCCTTGATGTCAGAGCTGGAAGAGAGGAGCACATCGCAGAAAGGGCCACTCTCGTTCTCTG	3665
Db	3415	CCCTTGATGTCAGAGCTGGAAGAGAGGAGTGGGTGGGCAAGAAACACCTCTCATCTGCTG	3474
Qy	3666	GAGACTAGCATAGATGGGATTTCTGGCTGATGTGAAGAACTCGAGAAACATTCAGAGACAC	3725
Db	3475	GAGACTAGCATAGATGGGATTTCTGGCTGATGTGAAGAACTCGAGAAACATTCAGAGACAC	3534
Qy	3726	CTGGCCCCGGGGCTCTCAATATCCAGAGCTCTTGAGCAACAGTGA 3770	
Db	3535	CTGGCCCCGGGGCTCTCAATATCCAGAGCTCTTGAGCAACAGTGA 3579	
RESULT 15			
AAC83734			
ID	AAC83734	standard; cdNA; 5057 BP.	
XX	AAC83734;		
XX	02-MAR-2001 (first entry)		
DT	Mouse laminin 5 cdNA, SEQ ID NO: 35.		
XX			
DE			
XX	Mouse; laminin 5; vulnerary; antituler; antinflammatory; antidiabetic;		
KW	cell adhesion promoter; wound healing; ulcers/ burn; skin graft;		
KW	periodontitis; gingivitis; Type I diabetes; angiogenesis regulation; ss.		
XX			
OS	Mus musculus.		
XX			
PN	WO200066731-A2.		
PD	09-NOV-2000.		
XX	28-APR-2000; 2000WO-US11459.		
PF			

XX 30-APR-1999: 99US-0131720.
PR 21-AUG-1999: 99US-0149738.
PR 24-SEP-1999: 99US-0155945.
XX
PA (BIOS-) BIOSTATUM INC.
XX
PI Boutaud A:
XX WPI: 2000-687538/67.
DR P-PSDB: AAB46473.
XX
XX Laminin 5-expressing cells, used to accelerate wound healing associated
PT with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
PR burns, acute wounds and skin grafts -
XX
XX Claim 4; Page 223-228; 232pp: English.
XX
XX The present sequence encodes a laminin 5 chain polypeptide. Recombinant
CC laminin 5-expressing cells are used to accelerate wound healing,
CC especially diabetic foot ulcers, venous ulcers, pressure sores, skin
CC surgery, burns, acute wounds, skin grafts, corneal ulcerations,
CC gastro-intestinal ulcers, periodontitis, and gingivitis. They are also
CC used to improve the biocompatibility of medical devices, and to promote
CC cell adhesion to a surface. They can be used for the ex vivo treatment
CC of Type I diabetes. Laminin can also be used to regulate angiogenesis.
CC The cell line produces and secretes recombinant heterotrimeric laminin,
CC whereas prior art cell lines have been created that produce but do not
CC secrete only one or two chain laminins.
XX
SQ Sequence 5057 BP: 1318 A; 1231 C; 1343 G; 1164 T; 1 other;
Query Match 63.6%; Score 2537.4; DB 21; Length 5057;
Best Local Similarity 83.0%; Pred. No. 0;
Matches 2944; Conservative 1; Mismatches 582; Indels 18; Gaps 4;
QY 261 ACCTCCGGAGGAGAGTCTGTGATGCAACGGAGATCCAGCAATGCATCTTGACAG 320
DB 1 ACCTCCAGAGGAGAGTCTGTGATGCAATGGAGATCCAGCAATGTCTTTGATCAG 60
QY 321 GAATCCACAAGACAGACAGAAATGATTCGGTCCCTCAACTGCATGACACACTGAT 380
DB 61 GAGCTCATCGACAGACAGAGCGAGGGGTTCCGTGCTCAACTGCATGACACATGACAGCG 120
QY 381 GGCATCCACTCGAGAGGTGCAAGGAGGATTTACGACAGAGAGAAAGGACCGCTGT 440
DB 121 GGGGTTCACGCGAGCGGTGAGGGAGGGGTTTACAGCATCAGAGCAAGACCGCGTGC 180
QY 441 TTACCTGCATTTGAACTGTAAGGTTCTTGTAGCGCTGATGACACTGTGACAGCG 500
DB 181 CTACCTGCAACTGCACTCAAAAGGTTCCCTCAGTGTGATGTGACAACTCTGACAA 240
QY 501 TGCAGCTGTAAAGAGGTGTGACAGAGACAGGTGTGACCGATGTGCGCGGCTTCAC 560
DB 241 TGCAGGTGTAAAGAGGTGTGACAGAGCAAGATGTGACAGGTGTGACAGCGGCTTCAT 300
QY 561 ACACTCACTGATGCTGGGTGCGCCCAAGACCAAGGCTGCTAGACTCCAACTGTGACTGT 620
DB 301 ATGCTCAACCGATGCTGAGTGCACCCAGACAGGCGCAACATGATTCGAACTGTGACTGT 360
QY 621 GACCAGCTGCACTGTCAGGCGCTGTGACTCAGGCGCTGTGCTGTGCAACCGGCTGTC 680
DB 361 GACCAGCTGCACTGTCAGGCGCTGTGACTCAGGCGCTGTGCTGTGCAACCGGCTGTC 420
QY 681 ACTGAGAGCGCTGTGATGATGTGTCAGACAGGTTATCACTGATGAGGAGAAACCTT 740
DB 421 ACTGAGAGCGCTGTGATGATGTGTCAGACAGGTTATCACTGATGAGGAGAAACCTT 480
QY 741 CAGGCTGTACCACTGTTTGTGATAGGCACTCCGCACTGCAAGCTCTGAGGAC 800
DB 481 GAGGCTGTACCACTGTTTGTGATAGGCACTCCGCACTGCAAGCTCTGAGGAC 540
QY 801 TACAGTGTCAATAATCATCTGTGCTTCCATCAAGATGTGATGCTGGAAGGCTGTC 860

DB 541 TTGAGTGTCCACAATAACACTTCAACTTGTAGTGCAGATGTGATGTTGGAAGCGGTT 600
QY 861 CAAGAAAGCGGTTCTCTGCAAGCTCCAGTGTGACAGCGGCAATGATATTTTAC 920
DB 601 CAGAGAAAGCGGCGGCACTGCAAACTCCAGTGTGACAGCGGCAATGATATTTTAC 660
QY 921 TCAGCAGAGATGAGACCGCTGTATTTGTACTGCTGCAAAATTTCTTGGAGATCA 980
DB 661 TGTGCGGAGATGAGACCGCTGTATTTGTGAGCGGCTGCAAAATTTCTTGGATACAG 720
QY 981 CAGGTGAGTACAGGCGCAAGGCTATCTTTGACTACCGGTGTGATGAGGAGGACAGAC 1040
DB 721 CAAGTGTATACGGGAGAGCGCTGCTTTGTGACTACCGGCGGAGAGGAGTATGACAG 780
QY 1041 CCATCTGCCATGACGTGATCTTGTGAAAGTCTGCTGACGATCAGACGCTCCCTGATG 1100
DB 781 CCGTCTGCTACGATGTGATCTGTGAAAGTCTGCTGACGATCAGAGCTCTCTGATG 840
QY 1101 CCAGTTGCAAGACACTGCGCTGTGAGATCACAAGACTTACATTCAGATTAATGAA 1160
DB 841 GCTCCAGGCAAGACACTTCTTGTGAGATCACAAGACTTACATTCAGATTAATGAA 900
QY 1161 CATCAGACACTAATGAGAGCGCCAGCTAAGTTACTTGTGATGAGAGGTTACTGCGG 1220
DB 901 CATCAGACACTAATGAGAGCGCGAGTCCAGCTGATTAATTCGAATTCGAAGGTTACTGCGG 960
QY 1221 AACTCAGAGC--CTGCGGATCCGAGACTACCTACGAGCAATACGATCTGAGTAT 1277
DB 961 AACCTCAGAGCCTCTGATGATGATCCGAGCTACGTAAGTAATGATGAGGTTACTAT 1020
QY 1278 GACAAGGATCTGATTTGAGCGCGCGCTTCTGAGAGCGCGCGCTGAGTGA 1337
DB 1021 GATTAACGAGCTGCTGTTGAGCGCGCGCTTCTGAGAGCGCGCGCTGAGTGA 1080
QY 1338 CAATGTGATGCGCTGTTGCTACAGAGGCGAGTCTGCGAGTGTCTTCCGCTAC 1397
DB 1081 CGTGTGATGCTGCTGCTGAGGCTACAGAGGCAATTCGCGAGATGCTGCTGATAC 1140
QY 1398 AAAAGATTCAGCGACAGCTGAGACCTTTTGGACACTGTATTCATGTAATCTGCCAAGG 1457
DB 1141 AAAAGATTCAGCGACAGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 1200
QY 1458 GAGAGGCGCTGAGTCCAGACAGAGAGACTGTAAGGAGGAGTGAACCTGAGATC 1517
DB 1201 GAGGAGCGCTGATCCAGACAGAGGAGATGCTACTGAGGAGAGAAATCTGACT- 1259
QY 1518 CCTGAGTGTGCTGACTGCGCCCATTTGTTTCTACAAAGATCCCAAGACCCCGAGCTGC 1577
DB 1260 --TGAGTGTGCTGACTGCTGCGCATCGGTTTCTACAAATGACCAATGAGACCCCGAGCTGC 1317
QY 1578 AAGCGTGCCTCTGCTGCAATGAGTGTGACTGCTGCTGATGCTGAGACAGAGAGGTG 1637
DB 1318 AAGCATGTGCTGCTGCAAAATGAGTGTGACTGCTGCTGAGTGTGAGACAGAGAGGTG 1377
QY 1638 GTGTGCAATTAATGCTGCGCCAGAGGTGTCACTGCTGCGGCTGAGTGTGCTGAGTGTG 1697
DB 1378 GTGTGTAACAATGCTGCGCCAGAGGTGTCACTGCTGCGGCTGAGTGTGCTGAGTGTG 1437
QY 1698 TATTTTGGGAGACCCCTTGTGAGGAGTGTGAGGCTGCTGAGGCTGCTGAGTGTG 1757
DB 1438 TTTCTTTGGGAGTCCCTTTTGGGAGTGTGAGGCTGCTGAGGCTGCTGAGTGTG 1497
QY 1758 AACAAACAAGTGTGAGACCTGAGTGTGCGGAGTGTGAGACCGCTGACAGAGGAGTGTG 1817
DB 1498 AACAAACAAGTGTGAGACCGCAATGCTGTGAGTGTGAGACCGTGTGAGAGGAGTGTG 1557
QY 1818 AAGTGTATCCAAACAAGTGTGAGGCTGACGTGTGACAGAGTGTGAGGAGGCTGACTATG 1877
DB 1558 AAGTGTATCCAAACAAGGCGGCTGTGACTGTGACAGTGTGACAGGAGTGTGAGTGTG 1617
QY 1878 GACCGTTGCTGCCAATCCAGACAGAGTGTGAGGCTTCAACTGCAACCGAGTGTG 1937

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 04:09:53 ; Search time 5205 Seconds
(without alignments)
12411.873 Million cell updates/sec

Title: US-10-053-662a-1

Perfect score: 3989
Sequence: 1 tgggtctctctattccacag.....ccagataatgcttattg 3989

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estlin:*
- 4: em_estlinu:*
- 5: em_estloy:*
- 6: em_estlpl:*
- 7: em_estlo:*
- 8: em_hlc:*
- 9: gb_estl:*
- 10: gb_est2:*
- 11: gb_hlc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: gb_gss:*
- 18: em_gss_hum:*
- 19: em_gss_inv:*
- 20: em_gss_pln:*
- 21: em_gss_vit:*
- 22: em_gss_fun:*
- 23: em_gss_mam:*
- 24: em_gss_mus:*
- 25: em_gss_other:*
- 26: em_gss_pro:*
- 27: em_gss_rnd:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	621	15.6	769	12	BG679084 602627037
2	609.4	15.3	919	12	BG679408 602627409
3	603.8	15.1	973	14	BQ687091 BQ687091
4	586.8	14.7	872	14	BQ686460 BQ686460
5	582	14.6	1007	12	BG749494 602707627
6	562.8	14.1	782	12	BG679991 602626709

	7	530	13.3	763	13	B1149191
	8	524.2	13.1	936	12	BG175669
	9	517.2	13.0	674	9	AL710184
	10	516.6	13.0	945	12	BG423903
	11	499.4	12.5	662	9	AI701039
	12	493.8	12.4	687	12	BE744593
	13	489	12.3	791	13	BG918341
	14	488.2	12.2	774	12	BF163600
	15	485.4	12.2	930	12	BG676601
	16	475.8	11.9	796	13	BM047745
	17	475.6	11.9	760	10	BB627917
	18	472.2	11.8	938	12	BF302784
	19	471	11.8	661	13	B1082572
	20	459.8	11.5	763	10	B114962
	21	456.4	11.4	978	12	BF100494
	22	456.2	11.4	667	10	BB617855
	23	450.8	11.3	626	14	BM849299
	24	447	11.2	617	12	BF081464
	25	442.6	11.1	538	10	BE032523
	26	442.4	11.1	596	13	BM538716
	27	435.6	10.9	561	12	BF564481
	28	429.2	10.8	536	13	BM044707
	29	414.8	10.4	624	10	BE005892
	30	407.2	10.2	819	13	B1691847
	31	406.2	10.2	656	10	BE311555
	32	401.6	10.1	507	10	AM369523
	33	398	10.0	697	12	BF320138
	34	386.2	9.7	590	14	BQ325079
	35	385.6	9.7	549	12	BF149296
	36	381.2	9.6	466	12	BF045508
	37	367.8	9.2	729	14	BM980789
	38	367	9.2	572	12	BF815018
	39	365.8	9.1	460	12	BE814142
	40	362.2	9.1	502	12	BF750814
	41	354.8	8.9	512	14	BQ312520
	42	346.6	8.7	458	12	BF747980
	43	344.8	8.6	404	12	BF874660
	44	341.2	8.6	447	12	BE813970
	45	341	8.5	457	14	BM836374

ALIGNMENTS

RESULT 1
LOCUS BG679084 769 bp mRNA EST 01-MAY-2001
DEFINITION 602627037F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4752080 5',
mRNA sequence.
ACCESSION BG679084
VERSION BG679084.1 GI:13910481
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 769)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaaps-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMU)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMU at:
http://image.llnl.gov
Plate: LAM10609 row: 1 column: 09
High quality sequence stop: 768.
location/Qualifiers
1. 769

FEATURES

source

Db 422 COTGATCTGATGACCAAGCTCTCTCAGTAGTAGAGAGAGGGGCTGTCTTACTGAGACA 481
QY 3563 GAAGCTTTTCCAGAGCAAGCTAGATCAACAGAGGAGGCTTGTATGTGAGACT 3622
Db 482 GAAGCTTTCCGAGAGCAAGACCCAGATATACAGGCACTGGGCCATGATGTACAGACT 541
QY 3633 GGAAGAGAGGGACATCGGAGAGAGGGCCACCTCCCTTCTGTGAGACTAGCATAGATG 3682
Db 542 GGAAGAGAGGGACATCGAGAGAGGGCCACCTCCATTTGCTGGAGACAGATAGATG 601
QY 3683 GATCTGCTGATGTGAGAAACCTGGAGAACATCAGGACCACTGGCCCGGCTGCTA 3742
Db 602 GATCTGCTGATGTGAGAAACCTGGAGAACATCAGGACCACTGGCCCGGCTGCTA 661
QY 3743 CAATACCCAGGCTCTTGAGCAACAGTGAAGCTGCTTGTAGATTTCTACACAGGCTCT 3802
Db 662 CAATACCCAGGCTCTTGAGCAACAGTGAAGCTGCTTGTAGATTTCTACACAGGCTCT 721
QY 3803 TGGGATTCAGACCTAGCTGCTTGTAGATTTCTCTCA 3837
Db 722 TGGGATTCAGATCTCAGGAGGCTGGAGGACCATGTCA 756

RESULT 3
B0687091 973 bp mRNA linear EST 15-JUL-2002
LOCUS AGENCOURT 8034003 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6208015
DEFINITION 5' mRNA sequence.
ACCESSION B0687091
VERSION B0687091.1 GI:21812420
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM2365 row: a column: 08
High quality sequence stop: 694.
Location/Qualifiers

FEATURES

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6208015"
/clone_lib="NIH_MGC_110"
/tissue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pOTB7, Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

BASE COUNT 289 a 217 c 279 g 179 t 9 others
ORIGIN

Query Match 15.1%; Score 603.8; DB 14; Length 973;
Best Local Similarity 82.4%; Pred. No. 9,4e-145;
Matches 740; Conservative 0; Mismatches 147; Indels 11; Gaps 4;

QY 2110 AGGCTCAGGTGAGACAGTACCAACGAGAGCTGGAAGGAGATGACAGAGGCTGAGC 2169
Db 2 AGGGTGGATGATGAGTACTACTGATATACAGAGCTGGAAGGAGATGACAGAGGCTGAGC 61
QY 2170 AGGCTTTCGGGACATTTCTGAGAGAGAGCCAGATTTCAAGAGATGCTTTAGATCTTCA 2229
Db 62 AGGCTTTCAGAGACATTTCTGAGAGATGCTGAGATTTCAAGAGTGTCTAGCAGATCTTTC 121
QY 2230 ATTCCTGGGTTGGCCCAAGGCAAGGACTCAAGAGATAGTACCGGGAGCCCTGGATGAGC 2289
Db 122 GTCTCAGTGTGGCCAGAGTGAAGAGCCCAAGAGAACAGTACAGGCGCTGGATGAGC 181
QY 2290 TCAAGATGACTGTGGAAGAGTTCGGGCTGCGGAGTCAATGCAATGCAAGCAAGTTCAGG 2349
Db 182 TCAAGATGACTGTGGAAGAGTTCGGGCTGCGGAGTCAATGCAATGCAAGCAAGTTCAGG 241
QY 2350 ATACTCGAGGCTCATCTACATGATGCGCTGAGCTTGAAGAGAGTACAGGCTTCCTTC 2409
Db 242 ATACTCGAGGCTCATCTACATGATGCGCTGAGCTTGAAGAGTACAGGCTTCCTTC 301
QY 2410 AAAACACCAACATTCCTCTTCAGGACACTAGTGGGCGCAAAATGGCTTAAAGTCTGG 2469
Db 302 GAAACACTACATTTCTCTGCTCAGACACTAGTGGGCGCAAAATGGCTTAAAGTCTGG 361
QY 2470 CTCAGAGGCGCAGAGATTTGGCAGACAGCCATGTTCACTCAGCCAGTAACTGAGCAAC 2529
Db 362 CTCAGAGGCGCAGAGATTTAGCAGAAACCCAGCTTGAATCAGCCAGTAACTGAGCAAC 421
QY 2530 TGGCAAGAGAAACCCAGAGATTTCCAAAGAGCTGATGCTACTGTGCGGAGCTTCGC 2589
Db 422 TGACAAAGGAAACTGAGACTATTCACAAAGCCCTCTCACTGTGCGGAGGCGCTTCG 481
QY 2590 AGGAGGAG-----GCGGAACCGGACCTCTGAGAGAGCCCTGCTGCAAGAGCTTGG 2643
Db 482 ATGAAGGAGTGGGAAGCGGAAGCGGTACCCGAGGTGTGTGTGCAAGGCTTGG 541
QY 2644 GAAATTTCCAGAAACTAAATCTTGCGCCAGAGATTTCTGAGGAGGCGCAACCAACCG 2703
Db 542 AAAATTTGAGAGAAACCAAGTCCCTGCGCCAGATTTGACAAAGGAGGCGCACTCAAGCG 601
QY 2704 ACATGGAAGCAGATAGTCTTATTCAGCATAGTCTCACCTTCTCAATTCCTGTCAGA 2763
Db 602 AAATTTGAAGCAGATAGTCTTATTCAGCATAGTCTCACCTTCTGATTCAGTGTCTCGC 661
QY 2764 TTCAGGAGTCAATATATAGTCTTCAGAGT---AGAAGCGAAGGCTCAGACAAAG 2820
Db 662 TTCAGGAGTCAATATAGTCTTTCAGGAGTGAAGAGCAGAGAGATCAAAAG 721
QY 2821 CTGATTTCTCTCAAAACCGTGTGACTAGCATATGATGATTTCAAGCAGCGCAAGACA 2880
Db 722 CGGATTTCACTNCTCAGCTCGTGTACCCAGGCAATATGATCAAGCTACACAGAGA 781
QY 2881 ATCTGGGAACCTGGAGAGAAACCCGCGACCTCTTACAGATGGAAGAAATGG- GAGA 2939
Db 782 ATCTGGGAACCTGGAGAGAAAGAGCAGACAGCTCTTACAGATGGAAGAAATGGGAGAGA 841
QY 2940 CAGACATAGATGACTCT- GCTTTCCTGTCGCACTTGTCTTAACCAAGCCCAAGAA 2996
Db 842 GGAAGATCAGATCAGCTGCTGCTTCCCGTCCATCTTGTCTAANACAGAGACAGAGA 899

RESULT 4
LOCUS B0686460 872 bp mRNA linear EST 15-JUL-2002
DEFINITION AGENCOURT 8064560 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6206340
5' mRNA sequence.

ACCESSION B0686460
VERSION B0686460.1 GI:21811776
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 872)	NIH-MGC	http://mgc.ncl.nih.gov/	National Institutes of Health, Mammalian Gene Collection (MGC)	
	Unpublished (1999)		Contact: Robert Strausberg, Ph.D.	

FEATURES	Location/Qualifiers
source	1. .872

BASE COUNT	258 a	197 c	257 g	159 t	1 others
ORIGIN					

Oy	2644	GAAATTTGCAGAAAACCTAAATCTCTGGGCCCAGAGATTGTCCAGGAGAGACCACGCAAAACG	2703
Db	542	AAAAATTGGAGAAAACCAAGTCCTCTGGCCCAAGCAATTGACAAAGGAGGCCACTAACGCG	601
Oy	2704	ACATGGAAGCAGATAGGCTTTATCAGCATAGTCTCCACCTCTTCATATTCGGTGTCTAGA	2763
Db	602	AAATTTGAAGCAGATAGGCTTTATCAGCAACATCTCCGCTCTCGATTTCAGTGTCTCGGC	661
Oy	2764	TTTCAGGGAGTAAATGATCAGTCCCTTGGAGGT---AGAAAGCAAGAGGCTCAGCAAAAAG	2820
Db	662	TTTCAGGGAGTACGATCAGTCCCTTTCAAGTGGAGAAAGCAAAAGAGATTCAAACAAAAG	721
Oy	2821	CTGATTTCTCTCAACCGTGTGACTAAGCATATGATGATGAGTTCAAGCAGCGTCAAAAGCA	2880
Db	722	CGGATTTCACTCTCAAGCCTTGCTAACCAAGGCATATGATGATGAGTTCAACGCTACACAGAGA	781
Oy	2881	ATCA-GGGAAACCTGGGAAAGAAACCGCGAGCTCTTACAGATGTGGAAAGATGGAGGA	2939
Db	782	ATCTGGGAAACTGGAAAGAGAAAGACAGCAGCTCTTACAGAAATGGAAAAAGTGGGGA	841

RESULT	5
LOCUS	BCG749494
DEFINITION	BCG749494 1007 bp mRNA linear EST 15-MAY-2001 602707627.F1 NIH_MGC_43 Homo sapiens CDNA clone IMAGE:4844167 5', mRNA sequence.
ACCESSION	BCG749494
VERSION	BCG749494.1 GI:14060147
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens

FEATURES:	Location/Qualifiers
source	1. .1007

BASE COUNT	232 a	270 c	309 g	196 t
ORIGIN				

||||| 1410 GCCAGACTGGGAGCTTTGGACCTGATTCATGTAACCTGCAAGGGGGAGGGGCGCCGC 1469
Db 2 CCTTTGGGTACAAGGGGGCAATTCGCCAGATTTGCTTGTGCTACAAAGAGATTC 61
Oy 1410 GCCAGACTGGGAGCTTTGGACCTGATTCATGTAACCTGCAAGGGGGAGGGGCGCCGC 1469
Db 62 GCGAGACTGGGAGCTTTGGACCTGATTCATGTAACCTGCAAGGGGGAGGGGCGCCGT 121
Oy 1470 GATCCAGACACAGAGAGATTTGATTCAGGGGATGAGAACCTGACATCCCTGAGTGTCT 1529
Db 122 GATCCAGACACAGAGAGATTTGATTCAGGGGATGAGAACCTGACATCCCTGAGTGTCT 178
Oy 1330 GACTGCCCATTTGTTTCTACACAGATCCACAGACCCCGCAGCTGCAAGCCGTGCCCC 1589
Db 179 GACTGCCCATTTGTTTCTACACAGATCCACAGACCCCGCAGCTGCAAGCCATGTGCC 238
Oy 1590 TGTGCAATGGCTCAGCTGCTCGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 1649
Db 239 TGTATTAACGGGTTTACCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 298
Oy 1650 TGCCCCAGGAGTGTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1709
Db 299 TGCCCCAGGAGTGTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 358
Oy 1710 CCCTTGGGGAGACGTGGCCAGTGAAGGCTTGTGACCCCTGTGACCTGCAAGCAACAGCTG 1769
Db 359 CCCTTGGGGAGACGTGGCCAGTGAAGGCTTGTGACCCCTGTGACCTGCAAGCAACAGCTG 418
Oy 1770 GACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1829
Db 419 GACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 478
Oy 1830 AACACAGCTGGGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1889
Db 479 AACACAGCTGGGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 538
Oy 1890 CCCAATCCAGCAGACAGATGTGAGCTTGAATGCAACCCAGTGGGCTCGAGGCTGTG 1949
Db 539 CCCAATCCAGCAGCAGATGTGAGCTTGAATGCAACCCAGTGGGCTCGAGGCTGTG 598
Oy 1950 GAGTGTGAGATGAGTGTGAGCTTGTGCAAGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCT 2009
Db 599 GAGTGTGAGATGAGTGTGAGCTTGTGCAAGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCT 654
Oy 2010 CATCGGACAGTACAGCTGTCCAGCTTGTATATCAAGTGAAGTTCAGATGGATCAG 2069
Db 655 AGCATATGGAGATTCAGCTGTCCAGCTTGTATATCAAGTGAAGTTCAGATGGATCAG 714
Oy 2070 TTTATG-CAGCAGCTCCAGATC-CTGAGGCTCTGATTTGCAAGGCTCAGGGTGG- 2122
Db 715 TTTATGCGCAGCAGCTTCCAGCAATGAGGCTCTGATTTCAAGGCTCAGGGTGG- 774
Oy 2123 --ACAGTACCCAGCAGCAGCTGGAAGGAGAGT--CAGCAGGCTGAGACGCTT 2177
Db 775 GATGTAGTACTGATPACAGCTGCTGAGGCGAGAGAGTCCAGAAAGCTGACCCCT 834
Oy 2178 CGGAGCATTTCTGAGAGAGCCCAAGATTTCAAGATGCTGTTAGATCTTCAATCTCCG 2237
Db 835 CCAAG-GACAGTCCGAGAGAGAGCCCAAGATGCTGTTAGATCTTCAATCTCCG 893
Oy 2238 GTGGCCAGAGCAGTCAAGAGATAGTACCAGGAGC 2277
Db 894 GGGGCAAGGTGAGAGAGCCGAGAGAGAGTACGAGAGC 933

RESULT 6
Bg679991 782 bp mRNA linear EST 01-MAY-2001
LOCUS 602626709F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4751499 5',
DEFINITION Bg679991
ACCESSION Bg679991.1 GI:13911388
VERSION Bg679991
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS 1 (bases 1 to 782)
TITLE Unpublished (1999)
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: rstraubs@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.lnl.gov
Plate: LNLN10608 row: a column: 04
High quality sequence start: 6
High quality sequence stop: 781.
location/Qualifiers
1. 782
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4751499"
/clone_lib="NCI_CGAP_Skn4"
/tissue_type="squamous cell carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPOK6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 179 a 194 c 231 g 178 t
ORIGIN
Query Match 14.1%; Score 562.8; DB 12; Length 782;
Best Local Similarity 88.5%; Pred. No. 3.3e-134;
Matches 680; Conservative 0; Mismatches 77; Indels 11; Gaps 6;
Oy 1361 CAAGGGGAGATTCGCGCAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1420
Db 1 CAAGGGGAGATTCGCGCAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
Oy 1421 ACCTTTGGCAGCTGTATTCATGTAATGCAAGGGGAGGGGCTGCTGCTGCTGCTGCTGCTGCT 1480
Db 61 GCTTTGGCAGCTGTATTCATGTAATGCAAGGGGAGGGGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Oy 1481 AGGAGCTGTACTGAGGGATGAGAACCTTGACATCCCTGAGTGTGCTGCTGCTGCTGCTGCT 1540
Db 121 AGGAGA-TGTATTCAGGGATGAGAAATCTGACAT--TGAATGTGCTGCTGCTGCTGCTGCT 176
Oy 1541 TGGTTTCTACAGATTCACAA--GAGCCCGGAGCTGCAAGGCTGCTGCTGCTGCTGCTGCTGCT 1598
Db 177 TGGTTTCTACAGATTCACAA--GAGCCCGGAGCTGCAAGGCTGCTGCTGCTGCTGCTGCTGCT 236
Oy 1599 GGGTTACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1658
Db 237 GGGTTACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 296
Oy 1659 GGTGTACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1718
Db 297 GGGGTACACGGTGGCCGCTGTGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 356
Oy 1719 GAAGTGGCCAGAGAGAGCTTGTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1778
Db 357 GAACATGGCCAGAGAGAGCTTGTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 416
Oy 1779 GCTTCGGGAGATGTGACCGCTGACAGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 1838
Db 417 GCTTCGGGAGATGTGACCGCTGACAGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 476
Oy 1839 GGGGTCACTGTGACCACTGCAAGAGAGCTACTATGAGGAGCCCTTGGCTGCCATATCA 1898
Db 477 GGCATCTACTGCAACAGTGCAGAGAGCTACTTGGGGAGCCCATTTGGCTGCCATATCA 536

QY	1899	GCACAACAAGTGTGAGCTTGGCAACGTGCAGACGAGGGCTGCGAGACCTGTGGAGTGTGCA	1958
Db	537	GCAGACAAGTGTGAGCTTGGCAACGTGCAGACGAGGGCTGCGAGACCTGTGGAGTGTGCA	596
QY	1959	AGTATGGACAGCTGTGTTTGGCAAGCCAGAGGCTTTGGTGGCTTC-AGCTGTGACATGCGGC	2017
Db	597	AGTATGGACAGCTGTGTTTGGCAAGCCAGAGGCTTTGGTGGCTTC-AGCTGTGACATGCGGC	656
QY	2018	ACTGACCAAGCTGTGCTTGTCTTATCAAGTGAAGTTTACATGATCAG-TTTATGC	2076
Db	657	ATT---CAGCTGTCCAGCTTCTATTAACAAGTGAAGTTTACATGATGATCAGTTTATGC	713
QY	2077	AGCAGCTCCAGATCCTGGAGGCGCTGTGATTTTGAAGGCTCAGAGTGGAG	2124
Db	714	AGCAGCTCCAGATCCTGGAGGCGCTGTGATTTTGAAGGCTCAGAGTGGAG	761
RESULT 7			
LOCUS	BI149191	763 bp	linear
DEFINITION	602848711.F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5012330 5',		
ACCESSION	BI149191		
VERSION	BI149191.1	GI:14609192	
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 763)		
TITLE	NIH-MGC http://mgc.nci.nih.gov/ .		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgabs-remail.nih.gov		
	Tissue Procurement: Gilbert Smith, Ph.D.		
	cDNA Library Preparation: Life Technologies, Inc.		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)		
	DNA Sequencing by: Incyte Genomics, Inc.		
	DNA distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMNL at: http://image.lnl.gov		
	Plate: LMNL1063 row: e column: 03		
FEATURES	High quality sequence stop: 753.		
SOURCE	location/Qualifiers		
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	/strain="CZECH 1"		
	/db_xref="taxon:10090"		
	/clone="IMAGE:5012330"		
	/clone_lib="NCI CGAP Lu29"		
	/tissue_type="spontaneous tumor, metastatic to mammary. Stem cell origin"		
	/lab_host="DH10B"		
	/note="Organ: Lung; Vector: pCMV-SPORT6; Site:1: SalI; Site:2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"		
BASE COUNT	236 a 179 c 214 g 134 t		
ORIGIN			
Query Match	13.3%; Score 530; DB 13; Length 763;		
Best Local Similarity	82.7%; Pred. No. 9,8e-126;		
Matches 630; Conservative 0; Mismatches 130; Indels 2; Gaps 2;			
QY	2504	TCAGTCAGCCAGTACATGAGCACTGGCAAGAAACCCAGAGATATCCAAAGACT	2563
Db	2	TGAGCTCAGCTATATCAATGAGCAACTGAGCAAGGAAATCTAGGACTCTCAAAACAAGC	61
QY	2564	GATGTCACTGTGTGGCGAGGCTCTGCGAAGAGAGGCGGAGCGGACCTCGAGCGAGC	2623
Db	62	ACTTTCGTTGGCCCGCAAGGCTCTGAGTGTGAGAGAGCGGAAAGCGGCTTGTGACAGCTC	121

LOCUS	DEFINITION	ACCESSION	KEYWORDS	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Db	122	CGTGGTCAAAAGCGTTGGGGAAAAATTGCAGAAAACTAAATCTGTGGCCGAGGATGTC	263						
Db	122	CTGTGGTCAAAAGCGTTGGGGAAAAATTGCAGAAAACTAAATCTGTGGCCGAGGATGTC	181						
Qy	2684	GAGGAGAGGCGCCAGCAAAACCGAGATGTAAGAGTCTTATCAGCATAGTCTCCACCT	2743						
Db	182	AAGGAGAGGCGCCAGCAAAACCGAGATGTAAGAGTCTTATCAGCATAGTCTCCACCT	241						
Qy	2744	TCTCAATTCCTGTCTCAGATTCCAGGAGTCAATGATCAGTCTTTCGACAGTGAAGCGAA	2803						
Db	242	CCTGATTCCTGTCTCAGATTCCAGGAGTCAATGATCAGTCTTTCGACAGTGAAGCGAA	301						
Qy	2804	GAGGCTTCGACAAAAGGCTGATATCTCTCAACCCGTGTGACTTAAGCATATGATGAGT	2863						
Db	302	GAGATTCAGCAAAAAGGCTGATATCTCTCAACCCGTGTGACTTAAGCATATGATGAGT	361						
Qy	2864	CAAGCAGGTGCAAAACCAATCTGGGAAATCGGGAAAGAAACCCGGCAGCTCTTACAGAA	2923						
Db	362	CAGCAGGTGCGAAACCAATCTGGGAAATCGGGAAAGAAACCCGGCAGCTCTTACAGAA	421						
Qy	2924	TGGAAAGAAATGGGAGACAGACATAGATCAGATCAGTCTTCCGTCGCAACCTGCTAAAG	2983						
Db	422	TGGAAAGAAATGGGAGACAGACATAGATCAGATCAGTCTTCCGTCGCAACCTGCTAAAG	481						
Qy	2984	CAGAGCCCAAGAACACACTAAGTATGGGCAATGCCACTTTTATGAAGTTGAGAACATCTT	3043						
Db	482	CAGAGCCCAAGAACACCGCTAAGTATGGGCAATGCCACTTTTATGAAGTTGAGAACATCTT	541						
Qy	3044	AAAGATCTCAGAGAGTTTGACCTGACCTGACAGGTTGAGATTAAGAGACAGACCTGAAGAGC	3103						
Db	542	GAAGAACCTCCGAGAGTTTGATCTGACAGGTTGAGATTAAGAGAGACAGAGCTGAAGAGC	601						
Qy	3104	CATGAAGAGATCTCTCTCAATCAGCAGCAAGCTTGAAGGTGCGAGTGCAGAGCAAGAGCA	3163						
Db	602	CATGAAGAGATCTCTCTCAATCAGCAGCAAGCTTGAAGGTGCGAGTGCAGAGCAAGAGCA	661						
Qy	3164	AGCAGAACGACCTGGGAGAGTCTGCTGCGCAGCGCCAGAGGAGCAAAAGATCAGAGCA	3222						
Db	662	AGCAGAACGACCTGGGAGAGTCTGCTGCGCAGCGCCAGAGGAGCAAAAGATCAGAGCA	721						
Qy	3223	GGGAGAGCCCTGGGAGAGTCTGCTGCGCAGAGATAGACAGAGATGA 3263							
Db	722	GGGAGAGCCCTGGGAGATCAGCAGCGAGATAGAGCAGAGATGA 763							
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LOCUS	BG175669	602334661F2	NCI_CGAP_Mam1	Mus musculus	cDNA clone IMAGE:4457942 5'				
DEFINITION									
ACCESSION	BG175669								
KEYWORDS	BG175669.1	GI:12682372							
EST									
SOURCE	house mouse.								
ORGANISM	Mus musculus								
REFERENCE	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
AUTHORS	Emmariota; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus								
TITLE	1 (bases 1 to 936)								
JOURNAL	NIH-MGC http://mgc.ncl.nih.gov/								
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)								
	unpublished (1999)								
	Contact: Robert Strausberg, Ph.D.								
	Email: cgaops-re@mail.nih.gov								
	Tissue Procurement: Gilbert Smith, Ph.D.								
	cDNA Library Preparation: Life Technologies, Inc.								
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMU)								
	DNA Sequencing by: Incyte Genomics, Inc.								
	Clone distribution: MGC clone distribution information can be								
	found through the I.M.A.G.E. Consortium/IMG/IMG at:								
	http://image.lncl.gov								
	Plate: LAM10255 Row: 1 Column: 15								
	High quality sequence stop: 681.								

FEATURES
source
Location/Qualifiers
1. .936
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_image="4457942"
/clone_lib="NCI_CGAP_Mam1"
/tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-Sport6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

BASE COUNT 273 a 234 c 295 g 134 t

ORIGIN

Query Match 13.1%; Score 524.2; DB 12; Length 936;
Best Local Similarity 82.0%; Pred. No. 3.5e-124;
Matches 652; Conservative 0; Mismatches 138; Indels 5; Gaps 4;

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1 GGAACCTGGGAGAGAAACACGCGACCTTTACAGACGAAAGGATGAGACAGACTT 60
2947 CAGATCAGCTCTTCCCGTCCCAACCTTGTAAAGAGAGCCCAAGAGACCTAAGTA 3006
61 CAGATCAGCTCTTCCCGTCCCAACCTTGTAAAGAGAGCCCAAGAGAGCGCTAAGTA 120
3007 TGGGCAATGCCATTTTATGAAAGTGAACATCTTAAAGATCTCAGAGATTGACC 3066
121 TGGGCAATGCCATTTTATGAAAGTGAACATCTTGAAGACTCGAGAGTTGATTC 180
3067 TGGGCAATGCCATTTTATGAAAGTGAACATCTTGAAGACTCGAGAGTTGATTC 3126
181 TGGGCAATGCCATTTTATGAAAGTGAACATCTTGAAGACTCGAGAGTTGATTC 240
3127 GCCAGAAAGTTCAGAGTCCAGTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3186
241 GCCAGAAAGTTCAGAGTCCAGTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
3187 CTCTGCGGAGCGCCAGAGGCGCAAGATGCAAGCCAGAGAGAGAGAGAGAGAG 3246
301 CCACTGCGGAGCGCCAGAGGCGCAAGATGCAAGCCAGAGAGAGAGAGAGAGAG 360
3247 AGATGAGACAGAGATGAGAGTCTGAAGTTCGAAGCCAAATGTGACAGATGAGAG 3306
361 AGATGAGACAGAGATGAGAGTCTGAAGTTCGAAGCCAAATGTGACAGATGAGAG 420
3307 TGGCATGAGAGAGAGAGTGGGCACTCTGAAAGATGAGATGAGAGAGAGAGAG 3366
421 TGGCATGAGAGAGAGAGTGGGCACTCTGAAAGAGAGAGATGAGAGAGAGAGAG 480
3367 TGGCATGAGAGAGAGAGTGGGCACTCTGAAAGATGAGATGAGAGAGAGAGAG 3426
481 TGGCATGAGAGAGAGAGTGGGCACTCTGAAAGAGAGAGATGAGAGAGAGAGAG 540
3427 AGGCCCAAGAGTTTAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3486
541 AGGCCCAAGAGTTTAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
3487 ACACATGAGAGAGAGAGTTCACATCAATAGACAGAGAGAGAGAGAGAGAGAG 3546
601 ACACATGAGAGAGAGAGTTCACATCAATAGACAGAGAGAGAGAGAGAGAGAG 658
3547 TGAATCTACAGAGAGAGAGTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3606
659 TGAATCTACAGAGAGAGTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 715
3607 CCTTATGTCAGAGAGAGAGTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3666
716 CCTTATGTCAGAGAGAGAGTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 775

QY 3667 AGACTAGCATAGATG 3681
DB 776 GAACACCCAGATTTG 790

RESULT 9
AL710184
LOCUS
DEFINITION DKFZp686J1267.1 686 (synonym: hicc3) Homo sapiens cDNA clone
ACCESSION AL710184
VERSION AL710184.1 GI:19693539
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 674)
Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and Wiemann
S.
EST (Duesterhoeft, et al.)
JOURNAL Unpublished (1995)
COMMENT Contact: Duesterhoeft A
MIPS
Am Klopferplatz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
consortium of the German Genome Project.
No sl sequence available.
This clone (DKFZp686J1267) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
source
Location/Qualifiers
1. .674
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="DKFZp686J1267"
/clone_lib="686 (synonym: hicc3)"
/tissue_type="human skeletal muscle"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pTriplex2; Site_1: SfiI; Site_2: SfiIb;
CDNA-collection"

BASE COUNT 146 a 190 c 204 g 132 t 2 others

ORIGIN

Query Match 13.0%; Score 517.2; DB 9; Length 674;
Best Local Similarity 88.3%; Pred. No. 1.9e-122;
Matches 597; Conservative 0; Mismatches 70; Indels 9; Gaps 3;

114 ACAGGAGAGCGCAGAGTGAAGAACTCCAGCGGAGAGCGGCGGAGAGAGAGAGAG 169
2 ACAGGAGAGCGCAGAGTGAAGAACTCCAGCGGAGAGCGGCGGAGAGAGAGAGAG 59
170 --CAGCGGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 227
60 GAGACAGAGACTGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 119
228 TGGCTTCTGCTCTCTCTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 287
120 TGGCTTCTGCTCTCTCTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 179
288 AACGGAGAGTCCAGAGTATGATCTTTGACAGAGAGTTCACAAACAGAGAGAGAG 347
180 AATGGAGAGTCCAGAGTATGATCTTTGACAGAGAGTTCACAAACAGAGAGAGAG 239
348 TTTCCGCTGCTTCACTGCAATGACAACTGATGAGAGAGAGAGAGAGAGAGAGAG 407
240 TTTCCGCTGCTTCACTGCAATGACAACTGATGAGAGAGAGAGAGAGAGAGAGAG 299
408 GGATTTTACAG 467

Db 300 GCGTTTACCGCAGACAGAGAGAGACCGCTGTTGCTCCGCAATGTATCTCAAGGTT 359
QY 468 TCTCTTAGCCGCTGATGTGACAACTGTGACGCTGACGTGTAAAGCAGGTGTACAGGA 527
Db 360 TCTCTTAGCTGCTGATGTGACAACTGCGGAGCGGTGACGTGTAAAGCAGGTGTACAGGA 419
QY 528 GACAGGTGTACCGAGTGTCTGCGCGGCTTCCACACACTGATGTGTGGTCCGCCAA 587
Db 420 GCGAGATGCGACCGAGTGTCTGCGGAGCTTCCACATGTCTGAGGTGGGTGACACCA 479
QY 588 GACCAAGGCTGTAGACTCCAGTGTGATGTGACCCAGCTGACATCTGAGGCGCTGT 647
Db 480 GACAGAGACTGTGACACTCCAGAGTGTGATGTGACCCAGCTGACATCTGAGGCGCTGT 539
QY 648 GACTCAGCGCGCTGTGTCTGCAAGCGGCTGTCTGATGTGAGAGAGCTGTGTAGTGTGCA 707
Db 540 GACGCGGCGCGCTGTGTCTGCAAGCGGCTGTCTGATGTGAGAGAGCTGTGTAGTGTGCA 599
QY 708 CCAGGTTACTATACCTGATGTGGGGAAACCTCTGAGGCTGTACCCAGTGTGTGTCTAT 767
Db 600 TCAGGTTACTATATATGTGATGTGGGGAAACCTCTGAGAGCTGTAT-CCAGTGTGTGTCTAT 658
QY 768 GGGCATTTCCGCCAGCT 783
Db 659 GGGCATTTCCGCCAGCT 674

RESULT 10
BG423903 945 bp mRNA linear EST 14-MAR-2001
LOCUS BG423903 602449854F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:4588548 5',
DEFINITION mRNA sequence.
ACCESSION BG423903
VERSION BG423903.1 GI:13330409
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE 1 (bases 1 to 945)
JOURNAL NIH-MGC http://imgc.ncl.nih.gov/
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1320 row: k column: 13
High quality sequence stop: 668.
Location/Qualifiers

FEATURES
source
1. 945

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4588548"
/clone_lib="NIH_MGC_14"
/tissue_type="renal cell adenocarcinoma"
/lab_host="pH10B (phage-resistant)"
/note="Organ: kidney; Vector: pOTB7; Site: 1; XhoI; Site: 2;
ECORI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT 231 a 236 c 280 g 198 t

Query Match 13.0%; Score 516.6; DB 12; Length 945;
Best Local Similarity 83.6%; Pred. No. 3.2e-122;
Matches 648; Conservative 0; Mismatches 114; Indels 13; Gaps 5;

QY 1653 CCCAGGCTGTCACTGTGCTCCCGCTGTGAGCTGTGTGTATGCTATTTTGGGACCCC 1712
Db 5 CCTCCCGGGGGTACCCTGCTCCCGCTGTGAGCTGTGTGTATGCTATTTTGGGACCCC 64
QY 1713 TTGCGGGGAACGTGGCCAGTGAAGGAGGCTGTGACCCCTGTGACCTGTGACCAACAGAGGAG 1772
Db 65 TTGCTGTGAACATGTGGCCAGTGAAGGAGGCTGTGACCCCTGTGACCTGTGACCAACAGAGGAG 124
QY 1773 CCTAGTCCCTCCGGGAATCTGTGACCCCTGTGACAGGAGTGTGTGAATGTCATCCACAC 1832
Db 125 CCCAGTGCCTCTGGGAATGTGTGACCCCGCTGACAGGAGGTGTGAATGTCATCCACAC 184
QY 1833 ACAGCTGGGTCCACTGTGTACCAAGTCAAGCAGGCTACTATGTGGACCCGTTGGCTCC 1892
Db 185 ACAGCCGGCATCTTACTGTGACCAAGTCAAGCAGGCTACTTCCGGGAGACCCATTGGCTCC 244
QY 1893 AATCCAGAGACAGTGTGAGCTGTGACCAAGTCAAGCAGGCTGTGAGGCTCCGAGCCTGGAG 1952
Db 245 AATCCAGAGACAGTGTGAGCTGTGACCAAGTCAAGCAGGCTGTGAGGCTCCGAGCCTGTGAG 304
QY 1953 TGTGGAAGTGTGAGCAGCTGTGTGTCAGAGCCAGGCTTTGTGCTCAGCTGTGAGCAT 2012
Db 305 TGTGGAAGTGTGAGCAGCTGTGTGTCAGAGCCAGATTTGTGTGCCCAACTGTGAGCAT 364
QY 2013 GCGGCACTGACCAAGCTGTGACGCTGTCTATATCAAGTGAAGTGTGATGATCACTTT 2072
Db 365 GGAAGCAT--CAGCTGTCCAGCTTCTATTAACAAAGTGAAGTGTGATGATCACTTT 421
QY 2073 ATGCACAGCTGCAGATCTGTGAGGCTCGATTTGCAAGGCTGAGG-----TGAGAGA 2126
Db 422 ATGCACAGCTGTGAGATGTGAGGCTCGATTTGCAAGGCTGAGGCTGATGATGAGTA 481
QY 2127 GTACCCAGCAGAGCTGTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 2186
Db 482 GTACCTGATTAACAGAGCTGTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 541
QY 2187 CTGAGAGAGAGCCCAATTTTCAACAAGTGTGTATGATCTTCAATTCCTCCGGGTGGCAAG 2246
Db 542 CTGAGAGAGTCCCAATTTTCAACAAGTGTGTATGATCTTCAATTCCTCCGGGTGGCAAG 601
QY 2247 GCAGAGCTCAAGAGATGTGACCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 2306
Db 602 TGA--GGAGCCAGAGAACGCTTACAGAGCCGCTGATGATGATGATGATGATGATGAT 659
QY 2307 AGAGTTGGGGCCCTGGG--CAGTCAATATGAG--AACCAAGTTCAGATCTGCGAGGCTCA 2364
Db 660 AGAGTTGGGGCTGTGGGAAGTCAATGACCAAGAACGAGTGGGATCTCCACAGAGTTTC 719
QY 2365 TCACGTAGATGGGCTGAGGCTGTGAGGAGAAAGTGAAGGCTTCCCTGCAAAACACCA 2419
Db 720 ATCATCATGTGAGGCTGAGGCTGTGAGGAGAAAGTGAAGTTCCTGCGGAAACCTTA 774

RESULT 11
A1701039/c 662 bp mRNA linear EST 17-DEC-1999
LOCUS A1701039 wc78a01.x1 NCI-CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2324712 3'
DEFINITION similar to SW-IMG2_HUMAN Q13753 LAMININ GAMMA-2 CHAIN PRECURSOR. ;
ACCESSION A1701039 GI:4988939
VERSION A1701039
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 662)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www.bio.lnl.gov/bbrp/image/image.html
Insert Length: 1025 Std Error: 0.00
Seq primer: -400P from Gldco
High quality sequence stop: 422.

FEATURES
source
1. .662
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2324712"
/clone_1id="NCI.CGAP_Pan1"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/note="Organ: pancreas; Vector: pCMV-Sport6; Site_1: Salt;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.72 kb. Life Technologies catalog #:
11548-013"

BASE COUNT 158 a 181 c 168 g 153 t 2 others
ORIGIN

Query Match 12.5%; Score 499.4; DB 9; Length 662;
Best Local Similarity 89.6%; Pred. No. 7.4e-118;
Matches 569; Conservative 0; Mismatches 63; Indels 3; Gaps 3;

OY 462 AAAGTCTCTTACGTCGATGACACACTGAGAGCGCAGCTGTAAGCCAGGTTG 521
DB 662 AAGGTTCTCTTACTGCTCGATGTG-CAGTCGGAANCGTGCAGCTGTAA-ACAGGTGTG 605
OY 522 ACAGAGACAGAGTGTGACCGATGCTGCGCGCTTCCACACACTCACTGATGCTGGTGC 581
DB 604 ACAGAGACAGATGACCGATGCTGCGCGCTTCCACATGCTACAGGATCGGNGGC 545
OY 582 GCCCAACACAAAGGCTGCTAGACTCCAGTGTGACTGTACCCAGCTGGCATCTCAGG 641
DB 544 -ACCAAGACCGAGAGCTGCTAGACTCCAAAGTGTGACTGTACCCAGCTGGCATCTCAGG 486
OY 642 CCTGTGACAGGCGGCTGTGTCGCAAGCGGCTGTACAGGAGCGCTGTGATAGG 701
DB 485 CCTGTGACGCGGCGGCTGTGTCGCAAGCGGCTGTACAGGAGCGCTGTGATAGG 426
OY 702 TGTGACACAGGTTACTATCAGCTGATGAGGGAACCTCCAGGCGCTTACCCAGTGT 761
DB 425 TGTGATCAGGTTACTATCAGCTGATGAGGGAACCTCCAGGCGCTTACCCAGTGT 366
OY 762 TGTGATGAGGTTACTATCAGCTGATGAGGGAACCTCCAGGCGCTTACCCAGTGT 821
DB 365 TGTGATGAGGTTACTATCAGCTGATGAGGGAACCTCCAGGCGCTTACCCAGTGT 306
OY 822 TGTGATGAGGTTACTATCAGCTGATGAGGGAACCTCCAGGCGCTTACCCAGTGT 881
DB 305 TGTGATGAGGTTACTATCAGCTGATGAGGGAACCTCCAGGCGCTTACCCAGTGT 246
OY 882 AAGTCCAGGTTACTATCAGCTGATGAGGGAACCTCCAGGCGCTTACCCAGTGT 941
DB 245 AAGTCCAGGTTACTATCAGCTGATGAGGGAACCTCCAGGCGCTTACCCAGTGT 186
OY 942 GTCTATTTTGTAGCTCTGCGCAATTTCTTGGGAATCAACAGGTGAGTACGGCAAGC 1001
DB 185 GTCTATTTTGTAGCTCTGCGCAATTTCTTGGGAATCAACAGGTGAGTACGGCAAGC 126
OY 1002 CTATCTTTGATACCGTGTGATGAGGGAACCACTCCAGGCGCTTACCCAGTGTATC 1061
DB 125 CTGTCTTTGATACCGTGTGATGAGGGAACCACTCCAGGCGCTTACCCAGTGTAT 66
OY 1062 CTGGAAGTGTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1096

Db 65 CTGGAAGTGTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 31

RESULT 12
LOCUS BE744593 687 bp mRNA linear EST 15-SEP-2000
DEFINITION 601577405p1 NIH_MGC_9 Homo sapiens CDNA clone IMAGE:3926472 5',
mRNA sequence.
ACCESSION BE744593
VERSION BE744593.1 GI:10158585
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 687)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: DCTD/DRP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
Plate: L10W754 Row: 1 Column: 01
High quality sequence start: 7
High quality sequence stop: 687.

FEATURES
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1. .687
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3926472"
/clone_1id="NIH_MGC_9"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: ovary; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; CDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCAGCAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 160 a 167 c 210 g 150 t
ORIGIN

Query Match 12.4%; Score 493.8; DB 12; Length 687;
Best Local Similarity 87.1%; Pred. No. 2.1e-116;
Matches 602; Conservative 0; Mismatches 77; Indels 12; Gaps 5;

OY 1584 TGCCCTTCCCAATGAGTGTAGCTGCTCCGATGAGCTGACAGAGAGGTGTGTC 1643
DB 2 TGTTCCTTCAATAGAGGTTTCACTGCTCAGTGAATGCGGAGAGAGGTGTGTC 61
OY 1644 -AATATGCCCCCAGGCTGATCTGTGCGCGCTGTAGCTCTGTGATGCTATTT 1702
DB 62 GAATTAAGTCCCTCCCGGGGTACCGCGGCTGTGAGCTGTGCTGATGCTACTT 121
OY 1703 TGGGAGCCCTTGGGGAACGTCGCGGAGTGAAGGCTGTGAGCCCTGTCAGTGAACAA 1762
DB 122 TGGGAGCCCTTGGGGAACGTCGCGGAGTGAAGGCTGTGAGCCCTGTCAGTGAACAA 181
OY 1763 CAAGTGAACCTTAAGTCTCCGGAATGTGACCGCGTGAAGGAGGAGTGTGAAGT 1822
DB 182 CAATGTGACCCCAATGCTCTGCGGAATGTGACCGCGTGAAGGAGGAGTGTGAAGT 241
OY 1823 CATCCACAACAGCTGGGCTCACTGTGACCAAGTGAAGAGGAGCTATGAGGAGCC 1882
DB 242 TATCCACAACAGCTGGGCTCACTGTGACCAAGTGAAGAGGAGCTATGAGGAGCC 301

FEATURES	source
REFERENCE	1883 GTTGGCTCCCAATCCAGAGCAAGTGTGACGCTTGCACAACTGCACCAACGAGTGGGCTCGGA 1944
AUTHORS	1883 GTTGGCTCCCAATCCAGAGCAAGTGTGACGCTTGCACAACTGCACCAACGAGTGGGCTCGGA 1944
TITLE	302 ATTGGCTCCCAACCCAGACAGACAGTGTGACGCTTGCACAACTGTATGCCCATGGGCTCGGA 361
JOURNAL	1943 GCCTGTGAGAGTGTGCAAGTGTATGTCAGCAGTGTGTGTTCACAGCCAGGCTTGTGTGCTCAG 2002
COMMENT	1943 GCCTGTGAGAGTGTGCAAGTGTATGTCAGCAGTGTGTGTTCACAGCCAGGCTTGTGTGCTCAG 2002
	362 GCCTGTGAGAGTGTGCAAGTGTATGTCAGCAGTGTGTGTTCACAGCCAGGCTTGTGTGCTCAG 421
	422 CTGTGAGATGAGAGCAATT--CACTGTTCACAGCTTGTATATCAATCAAGTGAATTCACAT 478
	2063 GGATCAGTGTATATGACAGCAGCTTCACATCTCTGGAGGCCCTGTGATTTTGCAGAGGCTCAGAGG-- 2119
	479 GGATCAGTGTATATGACAGCAGCTTCACAGATGTGAGAGGCCCTGTATTTCAAAGGCTCAGAGGTGG 538
	2120 ---TGGACAGTACCCCAAGCAGACAGTGTGGAAGGCGAGATGTCAGCAGCAGGCTGAGAGGCCCT 2176
	539 TGATGAGATGATGACTGTATACAGAGCTGTGAAGGCGAGATGTCAGCAGG--TGAGCAGAGGCCCT 597
	2177 TCGGACATCTTGTGAGAGAGAGCCAGATTTCAAGATGCTGTGTATATCAATCTCATCTCCG 2238
	598 TCAGACATCTTGTGAGAGATGTCAGAGTTCAGAAAGTGTCTGACAGATCCTTGTGTCTCA 657
	2237 GGTGGCCCAAGCAGCAAGTGTGGAAGGCGAGATGTCAGCAGCAGGCTGAGAGGCCCT 2267
	658 GTTGG--CAAGGTGAGAGGACCCCAAGAGCAAGC 687
RESULT 13	
LOCUS	BG918341 791 bp mRNA linear EST 05-JUN-2001
DEFINITION	60281963791 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:4948689 5',
ACCESSION	BG918341 mRNA sequence.
VERSION	BG918341.1 GI:14298817
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
	1 (bases 1 to 791)
	NIH-MGC http://mgc.nci.nih.gov/ .
	National Institutes of Health, Mammalian Gene Collection (MGC)
	Unpublished (1999)
	Contact: Robert Strusberg, Ph.D.
	Email: cgapbs-remail.nih.gov
	Tissue Procurement: Jeffrey Green M.D.
	cDNA Library Preparation: Life Technologies, Inc.
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
	DNA sequencing by: Incyte Genomics, Inc.
	Clone distribution: MGC clone distribution information can be
	found through the I.M.A.G.E. Consortium/LLNL at:
	http://image.llnl.gov
	Plate: LLAM10900 row: 1 column: 10
	High quality sequence stop: 758.
	Location/Qualifiers
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	/organism="Mus musculus"
	/strain="FVB/N"
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	/clone="IMAGE:4948689"
	/clone_lib="NCI CGAP Mam6"
	/sex="female, virgin"
	/tissue_type="infiltrating ductal carcinoma"
	/dev_stage="5 months"
	/lab_host="DH10B"
	/note="Organ: mammary; Vector: pCMV-SPORT6; Site1: SalI;
	Site2: NotI; Cloned unidirectionally. Primer: oligo dr.
	library constructed by Life Technologies. Investigator
	providing samples: Jeffrey Green, M.D., NIH"
BASE COUNT	226 a 190 c 231 g 144 t

[illegible]

REFERENCE
1 (bases 1 to 774)
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NIR-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
CONTACT: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLM9198 row: j column: 21
High quality sequence stop: 690.

FEATURES

Location/Qualifiers
1..774

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:3989108"
/clone_id="NCL.CGAP.Lu29"
/tissue_type="spontaneous tumor, metastatic to mammary."
/lab_host="DH10B"
/note="Organ: Lung; Vector: pCMV-Sport6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIR"

BASE COUNT 234 a 169 c 233 g 137 t 1 others
ORIGIN

Query Match 12.2%; Score 488.2; DB 12; Length 774;
Best Local Similarity 80.1%; Pred. No. 6.3e-115;
Matches 623; Conservative 0; Mismatches 149; Indels 6; Gaps 4;

OY 2545 AGGAGTATTCCTCAAGAGCTGATGTCACCTGTCGCGCGAGGCTCTCTCAGAGAGAGCGGAA 2604
DB 2 AGGACTACTCCAAACAGCACTTCTGTCGCGCGAGGCTCTCTCAGAGAGAGCGGAA 61
OY 2605 GCGGACACCTGGAGAGAGCGGCTGTGCAAAAGGCTGTGCAAAATTCGAGAACTAAT 2664
DB 62 GCGGCGCTTGGAGAGCTCCGCTGTACAGAGCTTTATGGAAATTTAGAGAAACCAAGT 121
OY 2665 CTCTGGCCAGAGAGTGTGAGAGGAGCCAGCAACCGACATGGAAGCAGATGATCTT 2724
DB 122 CCTGAGCCAGCAGCTGTCAAGGAGGAGCCCAAGCCGACATTTGAAGCTGATGTCAT 181
OY 2725 ATCAGCATATGCTCCACTCTTCAATTCGCTGTCAGATTCAGGAGTCAATGATCAGT 2784
DB 182 ATCAGCAGAGTCTCCGCTCTCAATTCGCTGTCAGATTCAGGAGTCAATGATCAGT 241
OY 2785 CCTTGCAGTGAAGAGAGGCTCAGAGCAAAAGGCTCTCTCTCAAAAGCTGTGA 2844
DB 242 CCTTGCAGTGAAGAGAGGCTCAGAGCAAAAGGCTCTCTCTCAAAAGCTGTGA 301
OY 2845 CTAGCATATGATGATGATTCAGAGCAGTCAAGCAATCTGGAAACTGGAGAGAGAA 2904
DB 302 CCAGCAAAACGAGTATTCACGCGGTGCGAAACATCTGGGAACTGGAGAGAGAA 361
OY 2905 CCGGCGAGCTCTTCAAGAAATGGAAGATGGAGAGACATCAGATCAGTCTTCC 2964
DB 362 CAGGCGAGCTCTTCAAGAAATGGAAGATGGAAGACATCAGATCAGTCTTCC 421
OY 2965 GTGCGAAGCTTCTTAAAGAGAGCCAGAGAGCACTAATGATGGCAATCCCACTTTT 3024
DB 422 GTGCGAAGCTTCTTAAAGAGAGCCAGAGAGCACTAATGATGGCAATCCCACTTTT 481
OY 3025 ATGAAGTTGAGACATCTTAAAGATCTCAGAGAGTTGACCTCAGGTTGAGAGTAA 3084
DB 482 ATGAAGTTGAGACATCTTAAAGATCTCAGAGAGTTGATC -TGAGTTGAGAGAGAA 539

OY 3085 GAGCAGAGCTGAAGAGAGCCATGAGAGACTCTCTACATCAGCCAGAGTTCCAGTG 3144
DB 540 AAGCAGAGCTGAAGAGAGCCATGAGAGACTCTCTATTTAGCCAGAGTTCCAGATG 599
OY 3145 CCACTGACAG 3204
DB 600 CCACTGACAG 657
OY 3205 GGGCAAGATGAG 3264
DB 658 GGGCAAG 716
OY 3265 GAGGTC-TGAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3321
DB 717 GGGGCTTGAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 774

RESULT 15

BG676601

LOCUS 930 bp mRNA Linear EST 01-MAY-2001
DEFINITION 602623078F1 NCL.CGAP.Skn4 Homo sapiens cDNA clone IMAGE:4748298 5',
mRNA sequence.

ACCESSION

BG676601

VERSION

BG676601.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 930)
NIR-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
CONTACT: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLM10599 row: k column: 19
High quality sequence start: 6
High quality sequence stop: 722.

FEATURES

source

Location/Qualifiers
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Query Match 12.2%; Score 485.4; DB 12; Length 930;
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Matches 707; Conservative 0; Mismatches 171; Indels 19; Gaps 10;

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 04:11:53 ; Search time 169 Seconds
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Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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Sequence 12, Application US/08317450B
Patent No. 5660982
GENERAL INFORMATION:
APPLICANT: Tyggvason, Karl
APPLICANT: Kallunki, Pekka
TITLE OF INVENTION: Laminin Chains: Diagnostic and
TITLE OF INVENTION: Therapeutic Use
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESSEE: BANNER & ALLEGRETTI, LTD.
STREET: Ten South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/317,450B
FILING DATE: 04-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Chao, Mark
REGISTRATION NUMBER: 37,293
REFERENCE/DOCKET NUMBER: 94,778
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
INFORMATION FOR SEQ ID NO: 12:
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LOCATION: 4433


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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Chao, Mark
REGISTRATION NUMBER: 37, 293
REFERENCE/DOCKET NUMBER: 94, 778-B
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
INFORMATION FOR SEO ID NO: 12:
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; Sequence 130, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong


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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/317,450B
FILING DATE: 04-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Chao, Mark
REGISTRATION NUMBER: 37,293
REFERENCE/DOCKET NUMBER: 94,778
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
INFORMATION FOR SEQ ID NO: 14:
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Db	2646	GCTTTATTCAGCACAGTCTCCGCCCTCTCGATTCAGTGTCTCCGCTCAGGGAGTCAATGA	2705
Qy	2780	TCAGTCCTTGGAGGT - - AGAAGGAAGAGGCTCAGACAAAACCTGATTTCTCTCAAA	2836
Db	2706	TCAGTCCTTTAGGTTGGAAGGAAGCAAAAGGATCAAAACAAAACGGATTCTACCTCAAG	2765
Qy	2837	CCGTGTGACTAAGCATTTATGATGATGATTCACACAGTCGACCAAAACATCTGGGAACTGGGA	2896
Db	2786	CCTGTATACCAAGGACATATGATGATGATTCACACGCTACACAAAAGAAATCTGGGAACTGGAA	2825
Qy	2897	AGAAAGAAACCCGGCAGCTCTTACAGATGGAAGAAATGGGAGACAGACATTCAGATCACT	2956
Db	2826	AGAAAGAACACAGCAGCTCTTACAGAAATGGAAAAAGTGGGAGACAGAAATCAGATCAAGCT	2885
Qy	2957	GCTTTCCGCTGCCAACCTTGTCTAAAGCAGAGCCCAAGAAAGCAGTAAGTATGGGCATATGC	3016
Db	2886	GCTTTCCGCTGCCCATCTTGTCTAAAGCAGAGCCACAAAGAACCTTGATATGGGCATATGC	2945
Qy	3017	CACCTTTTATGAAGTTGGAAACATCTTAAGAAATCTCAGAGAGTTTGACCTGCAGGTTGG	3076
Db	2946	CACCTTTTATGAAGTTGGAGACATCTTAAAAACCTCGAGAGATTGGACCTGCAGAGTGA	3005
Qy	3077	AGATTAAGACACAAAGCTGAAGAGGCCATGAAGACTCTCTCTACATCACCAGAAAGCT	3136
Db	3006	CACAGAAACACAGAAAGCTGAAGAAAGCCATGAAGACTCTCTCTACATCACCAGAAAGGT	3065
Qy	3137	TGCAGAGTCCAGTGCACAGAGCAAGCAAGCAAGCAGCCCTGGGGCAGTGTCTGGCCGA	3196
Db	3066	TTTCAGATCCAGTGCACAAAGACCACAGCAAGCAAGAAAGGCCCTTGGGAGGCCGTGTGCTCGA	3125
Qy	3197	CGCCACAGAGGCCAAAGAAATGCAGCCACGAGGAGCCCTGGAGATCTCTGGCAAAGATAGACA	3256
Db	3126	TGCACAGAGGGCCAAAGAAATGGGGCCGGGGAGGCCCTGGAAATCTTCAGTGAATTTGAAACA	3185
Qy	3257	GGAGATAGAGAGTCTGAACCTTGGAAAGCCAAATGTGCACAGCAATGAGAGCCTTGGCCATGGA	3316
Db	3186	GGAGATTTGGAGACTCTGAACCTTGGAAAGCCAAATGTGCACAGCAATGAGAGCCTTGGCCATGGA	3245
Qy	3317	GAAGGAGCTGGCCACTCTGAAAAGTGAAGTGAAGAAAGTGGAAAGAGAGCTGTCAAGGAA	3376
Db	3246	AAAGGAGCTGGCCCTCTCTGAAGAGTGAAGATGAGGAAAGTGAAGAGAGAGCTGTCAAGGAA	3305
Qy	3377	GGAGCAGAGATTTGACATGATATGAGACGCACTGCAATGCTATTTGCAAGAGGCCCAAG	3436
Db	3306	GGAGCTGGAGTTTGACAGAAATGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG	3365
Qy	3437	AGTTGAAGACAGAGCAGAAATGCTGGAGTTACGATCCAAACACACACTCAACATTTGGA	3496
Db	3386	GGTTATATACAGAGAGCAGAAAGCGTGGGGTTTACAAATCCAAACACACTCAACATTTGGA	3425
Qy	3497	TGGCATCTTACACTTAATAG	3516
Db	3426	CGGCTCCTCGATCTGATGG	3445

RESULT 5
US-08-800-593-14
Sequence 14, Application US/08800593
Patent No. 6143505
GENERAL INFORMATION:
APPLICANT: Tryggvason, Karl
APPLICANT: Kallunki, Pekka
APPLICANT: Pyke, Charles
TITLE OF INVENTION: Laminin Chains: Diagnostic and
TITLE OF INVENTION: Therapeutic Use
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive

CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,593
FILING DATE: 18-FEB-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/317,450
FILING DATE: 04-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Chao, Mark
REGISTRATION NUMBER: 37,293
REFERENCE/DOCKET NUMBER: 94,778-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
INFORMATION FOR SEQ. ID NO.: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 4316 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 118..183
FEATURE:
NAME/KEY: CDS
LOCATION: 118..3453
FEATURE:
NAME/KEY: repeat_unit
LOCATION: 4021..4316
OTHER INFORMATION: /rpt_type="other"
OTHER INFORMATION: /rpt_family="HUMAN ALU"
FEATURE:
NAME/KEY: polyA_site
LOCATION: 4296
US-08-800-593-14

Query Match 68.3%; Score 2726; DB 3; Length 4316;
Best Local Similarity 88.5%; Pred. No. 0;
Matches 3045; Conservative 0; Mismatches 365; Indels 30; Gaps 7;

QY 99 AAGGAAAGGAGGACAGCGGAGGAGAGTGAAGTCCACGCGGAGCGCGGCG 158
DB 14 AAGGAAAGGAGGACAGCGGAGGAGGAGTGAAGTCCACGCGGAGCGCGGCG 71
QY 159 AGGACCCCTGCAGCGCGC-----GACCGCGCGCGCGCGCGCATGCGCTCTG 211
DB 72 AGGACCCCTGCAGCGGAGGAGAGTGAAGTCCACGCGGAGCGCGCGCATGCGCTCTG 131
QY 212 GGTGACCTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 271
DB 132 GGTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 191
QY 272 GGAAGCTGTGATGGAAGGAGGAGTCCAGGCAATGCATCTTTGACGAGAACTTACA 331
DB 192 GGAAGCTGTGATGGAAGGAGGAGTCCAGGCAATGCATCTTTGACGAGAACTTACA 251
QY 332 ACAGACAGGAATGATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 391
DB 252 ACAGACAGGAATGATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 311
QY 392 CGAGAGGTGCAAGGAGATTTACCGAGAGAGAGAAAGGACCGCTGTTTACCTCGAA 451
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DB 312 CGAAGAGTCAAGATGCTTTTACCGGACAGAGAAAGGACCGCTGTTGCCCTGCA 371
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DB 372 TTCTACTCTAAGAGTTCTCTAGCCCTGATGTGACAACTGTGACGGGTGACGTGTA 431
QY 512 GCCAGGTGTGACAGAGAGAGGTGTGACGAGTGTGCCCGGCTTCCACACTCACTGA 571
DB 432 ACCAGGTGTGACAGAGAGAGGTGTGACGAGTGTGCCCGGCTTCCACACTCACTGA 491
QY 572 TGTGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 631
DB 492 TGTGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 551
QY 632 CATCTAGAGGCGCTGTGACTCAGCGCGCTGTGTCTGCAAGCCGCGCTGTGCTGAG 691
DB 552 CATCTAGAGGCGCTGTGACTCAGCGCGCTGTGTCTGCAAGCCGCGCTGTGCTGAG 611
QY 692 CTGTGATAGGTGTGACAGAGTTACTATCATCTGTGATGGGGAACCTCAGGGCTGTAC 751
DB 612 CTGTGATAGGTGTGACAGAGTTACTATCATCTGTGATGGGGAACCTCAGGGCTGTAC 671
QY 752 CGAGTGTGTTGCTATGGGCAATCCGCAAGCTGCGCACAGCTGCGGGAGTACAGTGTCA 811
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QY 1052 TGACGTGATCTGTGAGAGGTGTGTGTGATGAGGATCAGAGCTCCCTTATGCGACTT 1111
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DB 1032 GACACGCTGTGGGATCAGCAAGACTTACACATTCAGATTAATGAATCAAGCAAG 1091
QY 1172 TAATTTGAGCCCCCAGCTAAGTTACTTTGAGTATCGAGAGTTACTCGGAACTTCACAG 1231
DB 1092 TAATTTGAGCCCCCAGCTAAGTTACTTTGAGTATCGAGAGTTACTCGGAACTTCACAG 1151
QY 1232 CCTGCGGATCCGAGCTACGAGGAATACAGTACTGGGTACATTTGACAACTGACCTT 1291
DB 1152 CCTGCGGATCCGAGCTACGAGGAATACAGTACTGGGTACATTTGACAACTGACCTT 1211
QY 1292 GATTTCAGCGCGCGCTTTCTGAGAGCCGAGGCGCTGGGTGAACAATGTATGTGCC 1351
DB 1212 GATTTCAGCGCGCGCTTTCTGAGAGCCGAGGCGCTGGGTGAACAATGTATGTGCC 1271
QY 1352 TGTGAGCTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1411
DB 1272 TGTGAGCTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1331
QY 1412 CAGACTGTGACCTTTTGGCACTGTATTCATGTAACTGCCAAGGGGAGGGGCTGCGA 1471
DB 1332 GAGACTGTGACCTTTTGGCACTGTATTCATGTAACTGCCAAGGGGAGGGGCTGCGA 1391
QY 1472 TCCAGACAGAGAGATGTTTACTCAGGGGATGAGAACTTCGACATCCCGAGGTGCTGA 1531
DB 1392 TCCAGACAGAGAGATGTTTACTCAGGGGATGAGAACTTCGACAT--TGAGTGTCTGA 1448
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1532 CTGCCCATGTTGTTCTACAAAGATCCAAAGACCCCGACGTGCAAGCCGCTCCCTG 1591
1449 CTGCCCATGTTGTTCTACAAAGATCCGACAGACCCCGACGTGCAAGCCATGTCCTG 1508
1592 TCAGCAATGGTTTCAGCTGCTCCGTGATGCTGAGACAGAGAGGTGTGTCAATACGTG 1651
1509 TCATACAGGGTTTCAGCTGCTGATGATCCGAGACAGAGAGGTGTGTCAATACGTG 1568
1652 CCCCAGGGTGTCTCATGTTGCTCCGCTGTGACCTGTGCTGATGATGGCTATTTTGGGAGCC 1711
1569 CCGTCCCGGGGTGACCGGTGCTCCGCTGTGAGCTCTGTGCTGATGATGCTATTTGGGAGCC 1628
1712 CTTCGGGGAAAGCTGGCCAGTGAAGCCCTTGTACGCCCTGTGCTGAGTCAACAACAGTGA 1771
1629 CTTTGGTGAACATGGCCAGTAGAGCCCTTGTACGCCCTGTGATGCAACACCAATGTGA 1688
1772 CCTAGTGTCTCCGGGAACGTGTACCGCTGTACAGGACAGTGTCTGAATGTCATCCACAA 1831
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1832 CACAGCTGGGGTTCACAGTGTGACCAAGTGCAGAGGCTACTATGGGGACCGCTTGGCTCC 1891
1749 CACAGCGGACATCTACTGCGACAGTGCAGAGGCTACTTGGGGACCGCTTGGCTCC 1808
1892 CAATCCAGCAGACAAAGTGTGAGCTTGCACCTGCACACCAAGTGGGCTGAGACCTGTGA 1951
1809 CAACCCAGCAGACAAAGTGTGAGCTTGCACCTGTGAACCCATGGGCTAGAGCTGTAGG 1868
1952 GTTCGAAAGTGTGAGGACGTGTGTGTGCAACCCAGGCTTGGTGGCTCAGCTGTGACA 2011
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2012 TGCGGCACTGACAGCTGTGCTGCTATATCAAGTGAAGTGTGATGATGATGAT 2071
1929 TGGAGCAT--CAGCTGTGAGCTGTGCTATATCAAGTGAAGTGTGATGATGATGAT 1985
2072 TATCAGAGAGCTTCCAGATCCTGAGAGCCCTGATTTCCAAAGCTCAGG--TGGAGC 2125
1986 TATCAGAGAGCTTCCAGAAATGAGAGCCCTGATTTCCAAAGCTCAGGCTGTGATGAGT 2045
2126 AGTACCCAGCAGAGCTGGAAGGACAGATCAGACAGGCTGTAGCAGGCTTCCGGACAT 2185
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2186 TCTGAGAGAGCCAGATTTACAAAGATGCTTGAATCCTCAATCTCCGGGAGGCCAA 2245
2106 TCTGAGAGATCCCGATTTACAAAGGCTGTAGCAGATCCTTGGCTCCTCAGTTGGCCAA 2165
2246 GGCAGGACCTCAAGAGATAGCTACCGGACCGCTGATGACCTCAAGATGACTGTGA 2305
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2226 AAGAGTTGGGCTTGGGACGTCAAGTATCAACACCAAGTCAAGATCTCCAGGCTCAT 2285
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2286 CACATCAGATGAGCTGAGCTGTGAGAGAAAGTGAAGCTTCCCTGCAAAACACCAATCTCC 2345
2426 TCCCTCAGAGCAGTACGTGGGGCCAAATGGCTTTAAAAGTGTGGCTCAGAGGACGACAG 2485
2346 TGCCCTCAGAGCAGTACGTGGGGCCAAATGGCTTTAAAAGTGTGGCTCAGAGGACGACAG 2405
2486 ATTGGCAGACAGCAGTATCTTCAAGTCAAGCAGTACAGCAGTCAAGTCAAGGAAACCCA 2545
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2466 GGACTATTCAAAGAGCCCTCTCTCATGCTGTGGCAGAGGCTCTGCTATGAAGAGTGGAG 2525

2600 CGAAGCGGACGCTGACGAGGAGCGCTGTGCAAGAGCTTGTGGGAAATTTGCAGAAAC 2659
2526 CGGAAGGAGGTGACCGGAGCGTGTGTGTGCAAGGCTTGTGGAAATTTGAGAAAC 2585
2660 TAAATCTGTGGCCAGAGATTTGTGAGGAGGAGCCACCAACCATGAGAGAGATG 2719
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2706 TCAGTCTCTGAGGTGAGGAGAGGAGAGATCAACAAAGAGGATTCATCTCTCAAG 2765
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3257 GGAGTATGAGAGTGTGAACTTGAAGCCCAAGTGTGACAGAGTGTGAGGAGGAGGAGGAGGAGGAG 3316
3186 GGAGTATGAGAGTGTGAACTTGAAGCCCAAGTGTGACAGAGTGTGAGGAGGAGGAGGAGGAGGAG 3245
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3246 AAAGGAGTGTGCTCTGTGAAGAGTGAAGATGAGGAGAACTGTGAAGAGAGTGTGAAGGAA 3305
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3306 GGAGCTGAGAGTGTGACAGAGATGAGAGTGTGAGAGTGTGATTAAGAGGAGGAGGAGGAGGAG 3365
3437 AGTTGAAAGAGAGCAGAGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 3496
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RESULT 6
US-09-328-111-582/c
; Sequence 582, Application US/09328111
; Patent No. 6262333
; GENERAL INFORMATION:
; APPLICANT: Endege, Wilson O.
; APPLICANT: Steinhmann, Kathleen E.
; APPLICANT: Astle, Jon H.

```

; APPLICANT: Burgess, Christopher C.
; APPLICANT: Bushnell, Steven E.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Catino, Theodore J.
; APPLICANT: Dertli, Adnan
; APPLICANT: Ford, Donna M.
; APPLICANT: Lewis, Marcia E.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CCD-257 (US)
; CURRENT APPLICATION NUMBER: US/09/328,111
; CURRENT FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: US 60/088,801
; EARLIER FILING DATE: 1998-06-10
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 582
; LENGTH: 603
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(603)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-111-582

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Query Match      10.3%; Score 410.4; DB 4; Length 603;
Best Local Similarity 88.3%; Pred. No. 3.9e-108;
Matches 455; Conservative 0; Mismatches 59; Indels 1; Gaps 1;

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QY 812 TAAATATCATCTGCGCTTCATCAAGATGTGATGGCTGGAAGCGTGTCCAAAGAAAG 871
DB 455 TAAGATCATCTTNTACCTTATCAAGATGTGATGGCTGGAAGCGTGTCCAAAGAAAG 396
QY 872 GTCCTCTGCAAGAGCTCCAGTGTGACAGAGG -CCATGGGATATATTAGTCCAGCAGAC 930
DB 395 GTCTCTGCAAGAGCTCCAGTGTGACAGAGG -CCATGGGATATATTAGTCCAGCAGAC 336
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DB 335 GACTAGACCTGTCTATTTTGTAGCTCTGCAAGATTTCTTGGAAATCAACAGGTAGCT 276
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QY 1051 ATAGCATGATCTGGAAGGAGTGTGCTACAGATCAAGTCCCTTGATGCCACTAGCA 1110
DB 215 ATGATGTGATCTGGAAGGAGTGTGCTACAGATCAAGTCCCTTGATGCCACTAGCA 156
QY 1111 AGACACTGCTGTGGAGTACCAAGACTTACACATTCAGATTAAATGAATCAACAGCA 1170
DB 155 AGACACTGCTGTGGAGTACCAAGACTTACACATTCAGATTAAATGAATCAACAGCA 96
QY 1171 GTAAATGGAGGAGGAGGAGTGTGATGATGAGGAGTGTGAGGAGTGTGAGGAGTGTG 1230
DB 95 ATAAATGGAGGAGGAGGAGTGTGATGATGAGGAGTGTGAGGAGTGTGAGGAGTGTG 36
QY 1231 CCTGCGGATCGAGTACCTACGAGAAATACAGT 1265
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RESULT 7
 US-09-328-111-448
 ; Sequence 448, Application US/09328111
 ; Patent No. 6262333

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; GENERAL INFORMATION:
; APPLICANT: Endege, Wilson O.
; APPLICANT: Steinmann, Kathleen E.
; APPLICANT: Astle, Jon H.
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Bushnell, Steven E.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Catino, Theodore J.
; APPLICANT: Dertli, Adnan
; APPLICANT: Ford, Donna M.
; APPLICANT: Lewis, Marcia E.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CCD-257 (US)
; CURRENT APPLICATION NUMBER: US/09/328,111
; CURRENT FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: US 60/088,801
; EARLIER FILING DATE: 1998-06-10
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 448
; LENGTH: 551
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-328-111-448

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Query Match      9.7%; Score 388; DB 4; Length 551;
Best Local Similarity 84.6%; Pred. No. 1e-101;
Matches 462; Conservative 0; Mismatches 75; Indels 9; Gaps 2;

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QY 2332 ATCAGAACCAAGTTCAAGATCTCGCAGGCTCATCACTAGATCCGCTGAGGCTGAGG 2391
DB 1 ACCAGAACCGAGTTGGGATGATCAGAGGCTCATCACTAGATCCGCTGAGGCTGAGG 60
QY 2392 AAAGTAAAGCTTCCCTGCAAAACACCAACATTCCTCTTACAGCACTACGTGGGCCAA 2451
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QY 2452 ATGGCTTTAAAGTCTGGGCTCAGAGAGGCCAGGATTTGGCAGACACCAATGTTCACTAG 2511
DB 121 ATGGCTTTAAAGTCTGGGCTCAGAGAGGCCAGGATTTGGCAGACACCAATGTTCACTAG 180
QY 2512 CCAATTAACATGAGCAACTGCGCAAGGAAACCCAGAGATTTCCAAAGAGCTGATGTAC 2571
DB 181 CCAATTAACATGAGCAACTGCGCAAGGAAACCCAGAGATTTCCAAAGAGCTGATGTAC 240
QY 2572 TGGTGGCGGAGGCTCTGCAAGAGAGG -----GCGGAAGCGGACCTGAGAGGCGG 2625
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DB 301 TGGTGGCAAGAGGCTGTGGGAAATTCAGAAATCTGAGAAATCTGAGGAGGAGGAGG 360
QY 2686 GGGAGGCGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 2745
DB 361 GGGAGGCGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 420
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DB 421 TGGATTCAGTCTGCTGAGGAGTCAAGGAGTCAAGGAGTCAAGGAGTCAAGGAGTCAAG 480
QY 2803 AGAGGCTCAAGCAAAAGGAGTGTCTCTCAAAAGGAGTGTCTCTCAAAAGGAGTGTCT 2862
DB 481 AGAGGATCAAAAGGAGGAGTGTCTCTCAAAAGGAGTGTCTCTCAAAAGGAGTGTCT 540
QY 2863 TCAAGC 2868
DB 541 TCAAGC 546

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RESULT 8
US-09-221-298-26
; Sequence 26, Application US/09221298
; Patent No. 6284241
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER
; FILE REFERENCE: 210121.471
; CURRENT APPLICATION NUMBER: US/09/221.298
; CURRENT FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 401
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (219)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (236)
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; LOCATION: (276)
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; FEATURE:
; NAME/KEY: modified_base
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; OTHER INFORMATION: Where n is a, c, g or t
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; NAME/KEY: modified_base
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; FEATURE:
; NAME/KEY: modified_base
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; NAME/KEY: modified_base
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; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (330)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (335)
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; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (359)
; OTHER INFORMATION: Where n is a, c, g or t
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; NAME/KEY: modified_base
; LOCATION: (374)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (390)
; OTHER INFORMATION: Where n is a, c, g or t
US-09-221-298-26

Query Match 3.5%; Score 140.8; DB 4; Length 401;
Best Local Similarity 85.7%; Pred. No. 1,1e-30;

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Matches 168; Conservative 0; Mismatches 27; Indels 1; Gaps 1,
QY 3314 GGAGAGGAGCATGCGCCACTCTGAAAGTAGATGAGAGAGAGGAGAGAGCTGTCAAG 3373
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 GGAAGAGGAGCATGCGCCCTCTCTGAAAGTAGATGAGAGAGGAGAGAGCTGTCAAG 60
QY 3374 GAAGAGCAGCAGAGTTTACATGGAATATGAGAGCAGTCGACAGTGAATTTCACAGGCCA 3433
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 GAAGAGCAGCAGAGTTTACATGGAATATGAGAGCAGTCGACAGTGAATTTCACAGGCCA 120
QY 3434 AAGAGTTGAAAGACAG-AGCCAGAAGATCTGAGTTACGATCCAAAGACACACTCAACAT 3492
    | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 GAAGTTGATATCCAGGAAGCCAGAGACGCTGGGTTACAAATCCAGACACTCAACAT 180
QY 3493 TGGATGGCATCTTACA 3508
    || || || |||||
Db 181 TAGACGGGCTCTCTCA 196

RESULT 9
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHLITTLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZ9pt-F15
US-08-232-463-14
Query Match 2.0%; Score 79.2; DB 1; Length 7218;
Best Local Similarity 5.7%; Pred. No. 3,2e-12;
Matches 24; Conservative 245; Mismatches 153; Indels 0; Gaps 0;
3073 TTGGAGATAAAGACGAGACGCTGAAGAGCCATGAAGAGAGCTCTCTTACATCAAGCCAGA 31322

```


ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UC93-300-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1848 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 34..1845
US-09-136-981-1

Query Match 1.3%; Score 53.6; DB 4; Length 1848;
Best Local Similarity 52.1%; Pred. No. 3.3e-05;
Matches 147; Conservative 0; Mismatches 129; Indels 6; Gaps 1;

QY 156 GGCAGGAGACCCGACGAGCGGAGCCGCGCGCTGGCCATGCTGCTGCTGCTG 215
DB 931 GACAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 990
QY 216 AGCTGCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 275
DB 991 CCTTCACCTAGACCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1050
QY 276 GTGTGATTCACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 335
DB 1051 GCCTGTACTGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1110
QY 336 ACAGGA-----AATGATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 389
DB 1111 TCGGGGCGCAGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1170
QY 390 TGGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 431
DB 1171 TGGCATTACTGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1212

RESULT 14
US-08-482-677-7
Sequence 7, Application US/08482677
Patent No. 6017714
GENERAL INFORMATION:
APPLICANT: Tessier-Lavigne, Marc
APPLICANT: Serafini, Tito
APPLICANT: Kennedy, Timothy
APPLICANT: Placzek, Marysia
APPLICANT: Jessel, Thomas
TITLE OF INVENTION: Netlins
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,677
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UC93-300-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1811 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-482-677-7

Query Match 1.3%; Score 50; DB 3; Length 1811;
Best Local Similarity 57.9%; Pred. No. 0.00036;
Matches 110; Conservative 0; Mismatches 75; Indels 5; Gaps 1;

QY 247 CCGCAGCCCGGCGCACCTCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 306
DB 986 CCACGGCCCGCGAGGCCAAGAGTGGCTGCAACTGCAACTGCAACTGCTGCTGCT 1045
QY 307 GCATCTTTGACCGAGACTTCAACAACAGACAGG-----AATGATTCCTGCTGCTCA 361
DB 1046 GCAGATTCAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1105
QY 362 CTGCATGACACACATGATGAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 421
DB 1106 CTGCGCCGACACACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1165
QY 422 GAGAGAAAGG 431
DB 1166 CATGGGCAAG 1175

RESULT 15
US-08-482-677-5
Sequence 5, Application US/08482677
Patent No. 6017714
GENERAL INFORMATION:
APPLICANT: Tessier-Lavigne, Marc
APPLICANT: Serafini, Tito
APPLICANT: Kennedy, Timothy
APPLICANT: Placzek, Marysia
APPLICANT: Jessel, Thomas
TITLE OF INVENTION: Netlins
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,677
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UC93-300-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342

```

; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2779 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-482-677-5

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Query Match      1.3%; Score 50; DB 3; Length 2779;
Best Local Similarity 53.8%; Pred. No. 0.00046;
Matches 129; Conservative 0; Mismatches 105; Indels 6; Gaps 1;

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QY      185  CGCCGGGCTGCGCATGCGCTGCTGCTGAGCTGCTACCTGCTTCTGCTCTCTCT 244
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Db      860  CACCGAGGGGCGCCGAGTGGCGACCGCTGCAAGCCCTTCCACTACGACCGGCGGTGGCAGCG 919
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY      245  GCGCGGACGCCGGGCGCACCTCCGGGAGGGAAGTCTGTGATTGCAACGGGAAGTCCAGGCA 304
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      920  GGGCAGGCGCCGGGAGGCGCAACGAGTGCTGCGCTGCAACTGCACCTGCACGCTCGGCG 979
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY      305  ATGCATCTTGACCGAGGAACTTCACAACAGACAGG-----AATGATTCGCTGCT 358
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      980  CTGCGGCTTCAACATGAGGCTGTATTAAGCTGTCCGGCAGAGAGCGCGCGCTTTGCT 1039
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY      359  CAACGCAATGACAACAACATGATGATGCACTGCGAGAGGTCGAAGGCAAGATTATTACCG 418
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      1040  CAACGCGGACACACACAGCGGCTGGAGGCACTGCCACTACTGCAGAGGAGGCTTCTACCG 1099
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

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Search completed: July 6, 2003, 08:48:28
 Job time : 174 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 04:17:38 ; Search time 599 Seconds

(Without alignments)
10395.317 Million cell updates/sec

Title: US-10-053-662a-1

Perfect score: 3989

Sequence: 1 tgggtccctctattcacag.....ccagataaatgtcttattg 3989

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1085931 seqs, 780495707 residues

Total number of hits satisfying chosen parameters: 2171662

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA:*
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2: /cgn2_6/ptodata/2/pubpna/PCR_NEM_PUB.seq:*
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14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	2986.2	74.9	5200	9 US-10-227-738-12	Sequence 12, Appl
2	2986.2	74.9	5200	9 US-09-756-071B-12	Sequence 12, Appl
3	2972.8	74.5	5175	9 US-10-171-311-114	Sequence 114, App
4	2956.4	74.1	5156	9 US-09-466-386A-130	Sequence 130, App
5	2956.4	74.1	5156	9 US-09-735-705-130	Sequence 130, App
6	2956.4	74.1	5156	10 US-09-850-716A-130	Sequence 130, App
7	2956.4	74.1	5156	10 US-09-897-778-130	Sequence 130, App
8	2949.8	73.9	5460	12 US-10-044-090-558	Sequence 558, App
9	2726	68.3	4316	9 US-10-227-738-14	Sequence 14, Appl
10	2726	68.3	4316	10 US-09-756-071B-14	Sequence 14, Appl
11	515.6	12.9	4948	9 US-10-037-182-15	Sequence 15, Appl
12	515.6	12.9	5306	9 US-10-037-182-13	Sequence 13, Appl
13	515.6	12.9	7812	9 US-10-084-817-81	Sequence 81, Appl
14	515.6	12.9	7923	9 US-10-299-058-11	Sequence 11, Appl
15	515.6	12.9	7923	10 US-09-864-864-297	Sequence 297, App
16	514.6	12.9	7263	9 US-10-037-182-19	Sequence 19, Appl
17	514.6	12.9	7554	9 US-10-037-182-17	Sequence 17, Appl
18	514.6	12.9	8167	9 US-10-198-846-9785	Sequence 9785, Ap
19	420.8	10.5	613	10 US-09-998-598-1569	Sequence 1569, Ap

C	20	410.4	10.3	603	10 US-09-879-536-582	Sequence 582, App
	21	388	9.7	551	10 US-09-879-536-448	Sequence 448, App
	22	379	9.5	538	9 US-10-060-036-3398	Sequence 3398, App
C	23	366.8	9.2	551	9 US-10-076-622-248	Sequence 248, App
C	24	366.8	9.2	551	9 US-09-551-621-248	Sequence 248, App
C	25	366.8	9.2	551	10 US-09-604-287A-248	Sequence 248, App
C	26	366.8	9.2	551	10 US-09-339-338-248	Sequence 248, App
C	27	366.8	9.2	551	12 US-10-007-805-248	Sequence 248, App
	28	350.2	8.8	5184	10 US-09-845-583-9	Sequence 9, Appl
	29	332	8.3	458	9 US-10-060-036-840	Sequence 840, Ap
	30	265.2	6.6	1778	10 US-09-962-832-128	Sequence 128, App
C	31	218.8	5.5	262	12 US-10-033-528-1872	Sequence 1872, Ap
	32	161.2	4.0	188	9 US-10-025-380-696	Sequence 696, App
	33	161.2	4.0	188	10 US-09-922-217-696	Sequence 696, App
	34	161.2	4.0	188	10 US-09-833-263-696	Sequence 696, App
	35	160.6	4.0	221	10 US-09-998-598-2013	Sequence 2013, Ap
	36	140.8	3.5	401	9 US-10-025-380-26	Sequence 26, Appl
	37	140.8	3.5	401	10 US-09-922-217-26	Sequence 26, Appl
	38	140.8	3.5	401	10 US-09-833-263-26	Sequence 26, Appl
	39	132.2	3.3	579	9 US-10-084-817-82	Sequence 82, Appl
	40	109.8	2.8	129	10 US-09-998-598-1920	Sequence 1920, Ap
	41	86	2.2	9503	9 US-10-262-670-1	Sequence 1, Appl
	42	71.4	1.8	4837	10 US-09-764-877-2839	Sequence 2839, Ap
	43	71	1.8	9534	9 US-09-954-531-1380	Sequence 1380, Ap
	44	70.4	1.8	32250	9 US-09-764-891-9663	Sequence 9663, Ap
	45	70	1.8	781	10 US-09-764-877-2838	Sequence 2838, Ap

ALIGNMENTS

RESULT 1
US-10-227-738-12
Sequence 12, Application US/10227738
Publication No. US20030100529A1

GENERAL INFORMATION:
APPLICANT: Tryggvason, Karl
Kallunki, Pekka
Pyke, Charles
TITLE OF INVENTION: Laminin Chains: Diagnostic and
Therapeutic Use
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/227,738
FILING DATE: 26-Aug-2002
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/800,593
FILING DATE: 18-FEB-1997
APPLICATION NUMBER: US 08/317,450
FILING DATE: 04-OCT-1994

ATTORNEY/AGENT INFORMATION:
NAME: Chao, Mark
REGISTRATION NUMBER: 37,293
REFERENCE/DOCKET NUMBER: 94,778-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 5200 base pairs


```

1 ZIP: 4414
2
3 COMPUTER READABLE FORM:
4
5 MEDIUM TYPE: floppy disk
6
7 COMPUTER: IBM PC compatible
8
9 OPERATING SYSTEM: PC-DOS/MS-DOS
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11 SOFTWARE: PatentIn Release #1.0, Version #1.30
12
13 CURRENT APPLICATION DATA:
14   APPLICATION NUMBER: US/09/756,071B
15   FILING DATE: 08-Jan-2001
16
17 CLASSIFICATION: <unknown>
18
19 PRIOR APPLICATION DATA:
20   APPLICATION NUMBER: US 09/663,147
21   FILING DATE: 150-September 2000
22
23 ATTORNEY/AGENT INFORMATION:
24   NAME: Minnich, Richard, J.
25   REGISTRATION NUMBER: 24,175
26   REFERENCE/DOCKET NUMBER: TRV 20014
27
28 TELECOMMUNICATION INFORMATION:
29   TELEPHONE: 216-861-5582
30   TELEFAX: 216-241-1666
31
32 INFORMATION FOR SEQ ID NO: 12:
33
34 SEQUENCE CHARACTERISTICS:
35   LENGTH: 5200 base pairs
36   TYPE: nucleic acid
37   STRANDEDNESS: single
38   TOPOLOGY: linear
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40 MOLECULE TYPE: cDNA
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42 FEATURE:
43   NAME/KEY: sig_peptide
44   LOCATION: 116..183
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46 FEATURE:
47   NAME/KEY: CDS
48   LOCATION: 116..3699
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50 FEATURE:
51   NAME/KEY: polyA_site
52   LOCATION: 4433
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54 FEATURE:
55   NAME/KEY: polyA_site
56   LOCATION: 5195
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58 SEQUENCE DESCRIPTION: SEQ ID NO: 12:
59 US-09-756-071B-12
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OY	512	GCAGGTTGACAGGACGAGTGTGACGAAATGTCGCGGGTTCCACACATCCACGA	571
Db	432	ACCAAGTTGACAGGAGCCCAATGCGACCGATGTCGCCAGGCTTCCACATGCTCCACGA	491
OY	572	TGCTGGGTGCGCCCAAGACCAAGAGCTCTAGACTCCAAAGTGTGACTGTGACCCAGCTGG	631
Db	492	TGCGGGGTGCACCCCAAGACCCAGAGACTCTAGACTCCAAAGTGTGACTGTGACCCAGCTGG	551
OY	632	CATCTCAGGGCCCTGTGACTCAGGCGCGTGTCTGCGAAAGCGCGTGTCACTGAGACGG	691
Db	552	CATCGACAGGCGCCTGTGACGCGGCGCGTGTGTCTGCGAAAGCGCGTGTCTACTGTGAGAACG	611
OY	692	CTGTGATAGTGTGACAGCGTTACTATCACCTGGATGGGGGAAACCTTCAGGGCTGTAC	751
Db	612	CTGTGATAGTGTGATGATGAGTTACTATTAATCTGGATGGGGGAAACCTTCAGGGCTGTAC	671
OY	752	CCAGTGTCTTTTGTGATAGGGCAATTCGCGCAGCTGCCACAGCTCTGGGGACTACAGTGTCCA	811
Db	672	CCAGTGTCTTGTGATAGGGCAATTCAGCGAGTGCAGCTGTGCAAGTATCAGTGTCCA	731
OY	812	TAAATATCTCTGTGCTTCATCAAGATGTGATGGCTGGAAAGGCTGTCCAAAGAAACGG	871
Db	732	TAAATATCTCTGTGCTTCATCAAGATGTGATGGCTGGAAAGGCTGTCCAAAGAAATGG	791
OY	872	GTCCTCTGCAAAAGCTCCAGTGGTCCACAGCGCCATCGGGATATATTTAGCTCAGCAGCAG	931
Db	792	GTCCTCTGCAAAAGCTCCAGTGGTCCACAGCGCCATCAAGATGTGTTTAGCTCAGCCCAACG	851
OY	932	ATCAGACCCCTCATTTTGTGATGCTCCCGCCAAATTTCTGGGAAATCAACAGGTGAGCTA	991
Db	852	ACTAGATCTGTCTAATTTTGTGGCTCCGCGCCAAATTTCTGGGAAATCAACAGGTGAGCTA	911
OY	992	CGGGCAAAAGCTATCTTTTGTACTACCGTGTGATAGGGGAGGACAGACCCCATCTGCCCA	1051
Db	912	TGGGCAAAAGCTGTCTTGTACTACCGTGTGATAGGGGAGGACAGACCCCATCTGCCCA	971
OY	1052	TGAGTGTACTCTGGAAAGTGTGCTGTACGAGATCACAGCTTCCCTTGATGGCACCATTAGCA	1111
Db	972	TGATGTGTACTCTGGAAAGTGTGCTGTACGAGATCACAGCTTCCCTTGATGGCACCATTAGCA	1031
OY	1112	GACACTGCTGTGGGATCACCAAGACTTACACATTCAGATTAAATGACAACTCCACAGCAG	1171
Db	1032	GACACTGCTGTGGGATCACCAAGACTTACACATTCAGATTAAATGACAACTCCACAGCA	1091
OY	1172	TAAATGGAACCCCAAGCTAAGTACTTGTGAGTATGCGAGGTTACTCGGAAACCTCACAGC	1231
Db	1092	TAAATGGAACCCCAAGCTAAGTACTTGTGAGTATGCGAGGTTACTCGGAAACCTCACAGC	1151
OY	1232	CCTCGGATCCGAGCTACCTACGGGAAATACGACTAGTGGGATGTTGACAGCGTACACTT	1291
Db	1152	CCTCGGATCCGAGCTACCTACGGGAAATACGACTAGTGGGATGTTGACAGCGTACACTT	1211
OY	1292	GATTTACAGCCCGCTGTCTGTGAGGCCACCGCTGGGTTGAACAGTATATATGTC	1351
Db	1212	GATTTACAGCCCGCTGTCTGTGAGGCCACCGCTGGGTTGAACAGTATATATGTC	1271
OY	1352	TGTTGGCTACAAAGGGGAGTCTCCGAGAGTATGGCTTCGGGTCACAAAGAAAGATTCAGC	1411
Db	1272	TGTTGGCTACAAAGGGGAGTCTCCGAGAGTATGGCTTCGGGTCACAAAGAAAGATTCAGC	1331
OY	1412	CAGACTGGGACCTTTTGGACACTATTTCCATGTATACGTCCCAAGGGGAGGGGCTGTGGA	1471
Db	1332	GAGACTGGGACCTTTTGGACACTGTATTTCTGTATACGTCCCAAGGGGAGGGGCTGTGGA	1391
OY	1472	TCCAGACACAGGAGACTGTTACTCAGAGGGATGACAAACCTGTACATTCCTCTAGTGTCTGA	1531
Db	1392	TCCAGACACAGGAGACTGTTACTCAGAGGGATGACAAATCTGTACAT--TGAAGTGTCTGA	1448
OY	1532	CTGGCCCATTTGGTTTCTACAAAGATTCACAAAGACCCCGCAGCTGTCAAGCCGTGCCCTG	1591
Db	1449	CTGGCCCATTTGGTTTCTACAAAGATTCGACAGACCCCGCAGCTGTCAAGCCATGTCCCTG	1508

OY	1592	TCGCATATGGTTACAGCTGCTCCGTGATGCTTGACACAGAGAGAGTGGTGTGCATTAATCTG	1651
Db	1509	TCATTAAGGGGTTACAGCTGCTCAGTGAATTCGGAGACAGAGAGAGTGGTGTGCATTAATCTG	1568
OY	1652	CCCCCAGAGGTGCACTGTGGCCGCTGTGAGGCTGTGTGCGATGGCATTTTGGGGGCC	1711
Db	1569	CCCCGCCGGGGTCAACGGGTGCCCCGCTGTGAGGCTGTGTGATGAGCTTATTTGGGGGCC	1628
OY	1712	CTTTCGGGGAAAGTGGCCCCAGTAGAGCCCTTGTCAAGCCCCCTGTCACTGCAACAAACAACGTGGA	1771
Db	1629	CTTTGTGTGAACATGTGGCCAGTAGAGGCTTTGTCAACCCCTGTCAATGCAACAGCAATGTGGA	1688
OY	1772	CCCTAATGTCCTCGCGGAATCTGTGACCGCCTTGACAGCAGGTGTCTGAATGCATCCAA	1831
Db	1689	CCCCAGTGCCTCTGTGGGAATGTGTGACCGCGTAGACAGCAGGTGTTTGAAGTATCCAA	1748
OY	1832	CACAGCTGGGGTCCACTGTGACCGATCCAAAGCAGGCTACTATAGGGGAACCCGTGGGCTC	1891
Db	1749	CACAGCCGGGCACTTACTGTGCGACGATCCAAAGCAGGCTACTTCCGGGGAACCCATTGGCTCC	1808
OY	1892	CAATCCAGACAGACAAGTGTGAGCCTTGCACACTGCACACCAAGTGGGCTCGGAGCCTGTGGA	1951
Db	1809	CAACCCAGCAGACAAGTGTGAGCCTTGCACACTGTAAACCCATGGGCTCAGAGCCTGTGAG	1868
OY	1952	GTGTGCAAGTATGGCAGCTGTGTGTTTCCAAAGCCAGGCTTGTGGGCTCAGCTGTGAGA	2011
Db	1869	ATGTGCAAGTATGGCAGCTGTGTGTTTCCAAAGCCAGGATTTGTGTGGCCCAACTGTGAGA	1928
OY	2012	TGCGGCACTGACAGCCTGTCCAGCTTGTCTAATCAAGTGAAGTTCAAGATGATCAGTT	2071
Db	1929	TGAGGCACT---CAGCTGTCCAGGCTTCTAATAACAAAGTGAAGTATCAGATGATCAGTT	1985
OY	2072	TATCAGAGCTCCAGATCCCTGGAGAGCCCTATTTTCGAAGCCTCAAGG-----TGGAGC	2125
Db	1986	TATCAGAGCTTTCAGAGATGAGAGCCCTGATTTCAAGGCTCAAGGCTGTATGGAGT	2045
OY	2126	AGTACCCACAGCAGAGCTGGAAGCAGAGATGCACAGCAGCTGAGCAGGCCCTTCGGGACAT	2185
Db	2046	AGTACCTGATACAGAGCTGGAAGCAGAGATGCACAGCAGCTGAGCAGGCCCTTCAGAGAT	2105
OY	2186	TCTGAGAGAACCCAGATTTACAAAGATGCTTTAGATCCTTCAATCTCCGGGTGGCCAA	2245
Db	2106	TCTGAGAGATCCCCAGATTTTCAGAAAGGTGTACAGATCCCTTGTGTCCAGTGTGGCCAA	2165
OY	2246	GGCAAGGACCTCAAGAGATAGCTACCGGACCGGCTGTGATGACCTCAAGATAGATGTGGA	2305
Db	2166	GGTAGAGGCCCAAGAGAACACTTACAGAGCGGCTGTGATGACCTCAAGATAGATGTGGA	2225
OY	2306	AAGAGTTTCGGGCTGTGGGCACTGATACATCAACAACCAAGTTAGATACCTGCACAGCTCAT	2365
Db	2226	AAGAGTTTCGGGCTGTGGGAACTCACTACCAACAACCAAGTTGGGATACCTGCACAGCTCAT	2285
OY	2366	CAGTCAGATGCGCCTGAGCCTTGAGGAAGTGAAGCTTCCCTGCATAAACACCAACATYCC	2425
Db	2286	CAGTCAGATGCGCTGAGCCTTGAGGAAGTGAAGCTTCTTGGGAAACACTAACATYCC	2345
OY	2426	TCTCTCAGAGCACTACGTTGGGGCCAAATGGCTTTAAAAGTGTGGCTCAGAGGGCCACAG	2485
Db	2346	TGCTCTCAGACACTACGTTGGGGCCAAATGGCTTTAAAAGTGTGGCTCAGAGGGCCACAG	2405
OY	2486	ATTGGCAGACAGCATTTCTAGTCAGAGCCAGTAAACATGAGAGCAACTGGCAAGAAACCCA	2545
Db	2406	ATTGAGCAAAAGCCACGTTGATGATGAGCCAGTAAACATGAGAGCAACTGACAAAGAACTGA	2465
OY	2546	GGAGTATTTCCAAAGAGCTGATGTCACTGTGTGCGCGAGGCTTCAGAGGAAGAG-----G	2599
Db	2466	GGAGTATTTCCAAAGAGCTTCTACTGTGTGTGCGCAAGGCCCTGTGATGAAGAGTGTGAG	2525
OY	2600	CGGAAGCGGCAAGCTGTGAGAGGAGCCGTCGTGCAAAAGGCTTTGGGAAATTTGCAAGAAAC	2659
Db	2526	CGGAAGCGGTGAGCCGAGCGGTGTGTGTGCAAAAGGCTTTGTGGAATAATTTGTGAGAAAC	2585
OY	2660	TAAATCTCTGGCCCCAGAGTGTGTGAGGGAAGGCCACGCAACCAACATGAGAAGAGATG	2719

Db	2586	CAAGTCCCTGGCCCCAGAGATTGGACAAAGGAGGCCACATCAAGCCGGAATAATTGAAGCAGATAG	2645
QY	2720	GTCATTATCAGATATGTGCTCCACCTTCTTCATATTCGCTGTCCAGATATTCAGGAGATCAAT	2779
Db	2646	GTCATTATCAGACAGCTCTCCGCTCTCTTGATTCAGTGTCTCCGCTTTAGGAGAGCTCACTGA	2705
QY	2780	TCAGTCCCTTCAGAGT--AGAAGGGAAGAGGCTCAGACAAAAAAGCTGATTTCTCTCAAA	2836
Db	2706	TCAGTCCCTTCAGGATGGAAGAAGCAAGAGGATCAAAACAAAAGCGGATTCACGTCTAAG	2765
QY	2837	CCGTGTGACTTAAGCATATGATGATGATTCAGACACGTGCAAAACATTTGGGAAACTGGGA	2896
Db	2766	CCTGGTAAACCGGAGATATGATGATTCACACCGTACCAAAAAGATTTGGGAAACTGGAA	2825
QY	2897	AGAAAGAAACCCGGAGCTTACAGAAATGGAAGAAATGGGAGACAGACATTCAGATCAGCT	2956
Db	2826	AGAAAGAACACAGACAGCTCTTACAGAAATGGAAGAAATGGGAGAGAAATTCAGATCAGCT	2885
QY	2957	GCTTTCCCGTCCCAACCTTGTCTAAAGCAGAGCCCAAGAAAGCACTAAGTATGGGCAATGC	3016
Db	2886	GCTTTCCCGTCCCAATCTTGTCTAAAGCAGAGCAAGAAAGCACTGATATGGGCAATGC	2945
QY	3017	CACCTTTTATGAAAGTTGAGAACATCTTAAGAAATCTCAGAGAGTTTGACCTGCAAGTTTG	3076
Db	2946	CACCTTTTATGAAAGTTGAGAACATCTTAAAAAACCAGAAAGTTTGACCTGCAAGTTTG	3005
QY	3077	AGATTAAGACACAGAGCTGGAAGAGGCCATGACAGAGCTCTCCATCAATCACCAGAAAGT	3136
Db	3006	CACAGAAACACAGAGCTGGAAGAGGCCATGACAGAGCTCTCTACATCACCAGAAAGT	3065
QY	3137	TGCAGAGTCCAGTGCACAAGAGCAAGACAGAGCCCTGGGCGAGTGTCTGCTGCGGA	3196
Db	3066	TTCAATATCCAGTGCACAAGAGCCCAAGAGCAAGAAAGCCCTGGGAGAGCGTGTCTGCGGA	3125
QY	3197	CGCCAGAGGSCAAAAGATGCAAGCCAGGAGGCCCTGGAGATCTCTGGCAAGATAGACA	3256
Db	3126	TGCACAGAGGSCAAAAGATGAGGAGCCGCGGAGGCCCTGGAAATCTCCAGTGAATGGAACA	3185
QY	3257	GGAATATAGAGAGTCTGAACTTGGAAAGCCAAATGTGACAGCAATATGAGACCTTGGCGATGA	3316
Db	3186	GGAGATTTGGAGTCTGAACTTGGAAAGCCAAATGTGACACAAATATGAGACTTGGCGATGA	3245
QY	3317	GAAGGAGTGGGCACTGTGAAGAAGTGAATGAGAGAAATGGAAGAGAGCTGTCAAGAA	3376
Db	3246	AAAGGAGATGGGCTCTCTGGAAGAGTGAATGAGGAAAGTGGAAAGAGCTGTGGAAGAA	3305
QY	3377	GGAGCAGAGATTGACATGATATGAGCAGCAGTGCAGATGGTAAATTGCAGAGGCCCAAG	3436
Db	3306	GGAGCTGGAGTTTGACAGCAATATGATATGACAGATGGTGAATTACAGAAAGCCCAAG	3365
QY	3437	AGTTAAAAACAGAGCCCAAGATGCTGGAGTTTACGATCCCAACACACTCAACACATTTGGA	3496
Db	3366	GGTTTATACCAAGAGCCCAAGAGCGTGGGTTTACCAATCCAAACACACTCAACACATTTGGA	3425
QY	3497	TGGCATCTCTACACCTAATAGACAGACCGTGGCAGTGTGATGAAGAAGAGCGTGAATCTACT	3556
Db	3426	CGGCTCTCTGATCTGATGAGACCAAGCTCTCAGTGTGATATGAAGAGGAGCGTGTCTACT	3485
QY	3557	GGAGCAGAGCTTTTCCAGGCCAAGACTCAGATCAACAGCCAGCTAGCGGCTTGTGATGTC	3616
Db	3486	GGAGCAGAGCTTTTCCGAGGCCAAGACCAGATCAACAGCCAGCTAGCGGCTTGTGATGTC	3545
QY	3617	AGAGCTGAGAGAGAGGCGACATCGGAGAGAGGCGACCTCCGTTTCTCTGGAGACTAGCAT	3676
Db	3546	AGAGCTGAGAGAGAGGCGACCTGAGAGAGGCGCACCTCCATTTGCTGGAGAGCAAGCAT	3605
QY	3677	AGATGGAGTTCTGGGCTGATGTAAGAACTGTGAGAACTCAAGGGAACAACCTGCCCCGGG	3736
Db	3606	AGATGGAGTTCTGGGCTGATGTAAGAACTTTGAGAGCAACTTGGGGAACAACCTGCCCCAGG	3665
QY	3737	CTGCTACATATCCACAGGCTCTTGAGCAACAGTGAAGCTGCTTGAAGATTTCTCAACAA	3796

Db	1496	CTGCTCACTGATATGCCGGACGACGAGGAGAGTGTCTGCATAATTACTGCCCTCCCGGGGTAC	1553
OY	1667	TGCTGCCCGCTGTAGAGCTCTGTGCTGTAATGGCTATTTTGGGGACCCCTTCGGGGAACGTGG	1726
Db	1556	CGGTGCCCGCTGTAGAGCTCTGTGTAATGGCTACTTTGGGAGACCCCTTTGTGTAAACATGG	1615
OY	1727	CCCAATGAGGCTTTGTCAAGCCCTCTCACTGATGCACAAACACGTGGACCCCTAGTGCCTCGG	1786
Db	1616	CCCAATGAGGCTTTGTCAAGCCCTCTCACTGATGCACAAACACGTGGACCCCTAGTGCCTCGG	1675
OY	1787	GAATGTGACCGCTGACAGGCAAGGCAAGTGTCTGAAATGATCCACAAACACACTGGGGTCCA	1846
Db	1676	GAATGTGACCGCTGACAGGCAAGGCTTTGAAATGATCCACAAACACAGCGGGCACTTA	1735
OY	1847	CTGTGACCAAGTGCACAAACAGAGCTCTATATGGGAGACCCCTTGGCTCCCAATCCAGAGACAA	1906
Db	1736	CTGTGACCAAGTGCACAAACAGAGCTCTATATGGGAGACCCCTTGGCTCCCAATCCAGAGACAA	1795
OY	1907	GTTGTGACCTTGCACACTGCAACCCAGTGGGCTCGGAGCCTGTGAGTGTGCAAGTGTATGG	1966
Db	1796	GTTGTGACCTTGCACACTGTAACCCCATATGGGCTCAGAGCCTGTAGATGTGCAAGTGTATGG	1855
OY	1967	CAGCTGTGTGTGCAAGCCAGGCTTTGGTGGCTCAAGCTGTGAGCATCGGCACTGACACAG	2026
Db	1856	CACCTGTGTGTGCAAGCCAGGATTTGGTGGCCCACTGTGAGCATGTGAGCATTT--CAG	1912
OY	2027	CTGTCCAGACTTGCATATATCAAGTGAAGGTTCAAGTGAATGATGATAGTTTATGGCAGCGTCCA	2086
Db	1913	CTGTCCAGACTTGCATATATCAAGTGAAGGTTCAAGTGAATGATGATAGTTTATGGCAGCGTCCA	1972
OY	2087	GATCCTGGAGGCCCTGATTTTCGAAGGCTCAAGG-----TGGAGCACTATCCCAACGACGA	2140
Db	1973	GAGAAATGAGGCCCTGATTTTCGAAGGCTCAAGGCGTGTGATGTGAGTATGATCTGATACAGA	2032
OY	2141	GCTGGAAGGCAAGATGACAGCAGGCTGAGCAGGCGCTTCGGGACACTTCTGAGAGAACCCCA	2200
Db	2033	GCTGGAAGGCAAGATGACAGCAGGCTGAGCAGGCGCTTCAGAGCACTTCTGAGAGATGACCCA	2092
OY	2201	GATTTCAACAATGCTGTTAGATCTCTCAATCTCCGGGTGGCCCAAGGCAAGGATCTCAAGA	2260
Db	2093	GATTTCAACAATGCTGTTAGATCTCTCAATCTCCGGGTGGCCCAAGGCAAGGATCTCAAGA	2152
OY	2261	GAATAGCTACCGGGAGCCGCTGATGATGACCTCAAGATGACTGTGGAAGAGTTCGGGCGCT	2320
Db	2153	GAACAGCTACCGAGAGCGCCCTGATGATGACCTCAAGATGACTGTGGAAGAGTTCGGGCGCT	2212
OY	2321	GGGCAATGATATAGAAACAAGTTCAAGATATCTGCAAGGCTCACTCACTCAGATGCGCT	2380
Db	2213	GGGAAATGATATAGAAACAAGTTTCGGGATATCTCAAGGCTCACTCACTCAGATGCGCT	2272
OY	2381	GAGGCTGGAGAAAGTGAAGGCTTCCCGCAAAACCAACAATTCCTCTCAGAGCACTA	2440
Db	2273	GAGGCTGGAGAAAGTGAAGGCTTCCCGCAAAACCAACAATTCCTCTCAGAGCACTA	2332
OY	2441	CGTGGGGCCAATGGCTTTAAAGTCTGAGCTCAGAGAGCCACGAGATGTGCGACACACCA	2500
Db	2333	CGTGGGGCCAATGGCTTTAAAGTCTGAGCTCAGAGAGCCCAAGATTTAGACAGAAAGCA	2392
OY	2501	TGTTCAATGACCCAGTAATCATGAGACAACTGGCAAGAGAAACCAAGAGTATTTCCAAAGA	2560
Db	2393	CGTTGAGTCAAGCCAGTAATCATGAGAGCAACTGACAAAGGAAACTGAGGACCTATTTCCAAACA	2452
OY	2561	GCTATGTCATGTGGTGGCGGAGGCTCTGCAAGGAAGAG--GCGGAAGCGGACGCT	2614
Db	2453	AGCCCTCTCACTGTGGCGCAAGGCTCTGCAATGAAGGAGTCCGAAGCGGAACGGGTAGCCC	2512
OY	2615	GGAGGGAAGCCCTGTGTGCAAAAGCTTTGTGGAAAAATTGCAAGAAACTAAATCTTGCGCCA	2674
Db	2513	GGAGGGTCTGTGTGTGCAAGGCTTTGTGTGAAAAATTGCAAGAAACCAAGTCCCTTGCGCCA	2572
OY	2675	GGAGTGTGCAAGGAGGCGCACCAACCGCATGGAAGCAGATAGGTTTATTCAGATAG	2734
Db	2573	GCAGTTTCAAGAGGAGGCGCACTCAAGCGGAATTTGAAGCAATATGAGTGTATTCAGACAG	2632

QY	2735	TCCTCCACCTTCTCAATTCCGCTGTCTCAGATTCAAGGAGTCAATGATCATGCTCTTGCAAGT	2794
Db	2633	TCCTCCGCTCTCTGGATTCAGTGTCTCGGCTTCAAGGAGTCAAGTATCATGCTCTTGCAAGT	2692
QY	2795	-- -AGAAGCGAAGGGCTCAGACAAAAGCTGATTCTCTCTCAACCGCTGTGACTAAGCA	2851
Db	2693	GGAAGAAACCAAGAGGATCAACACAAAAGCGGATTTCACTCTCAACGCTGTGTAACABGCA	2752
QY	2852	TATGATGAGTTCAAGCAGTGCAAAGCAATCTGGGAAACTGGGAAAGAAACCCGGCA	2911
Db	2753	TATGATGAGTTCAAGCGTACACAAAAGAACTCTGGGAAACTGGGAAAGAAAGACACAGCA	2812
QY	2912	GCTCTTACAGAAATGGGAAGATGGGAGACAGACATCAAGTACAGTGGCTTCCCTGGCCAA	2971
Db	2813	GCTCTTACAGAAATGGGAAGATGGGAGAGAAATTCAGATCAGTGGCTTCCCTGGCCAA	2872
QY	2972	CCTTGCTTAAAGCAGAGCCCAAGAAAGCACTAAGTATGGGCAATGCCACTTTTATAGAGT	3031
Db	2873	TCTTGCTTAAAGCAGAGCACAAAGAAAGCACTAAGTATGGGCAATGCCACTTTTATAGAGT	2932
QY	3032	TGAGAACATCTTAAAGAACTCTCAGAGATTTGACCTGCAGGTTGGAGATTAAGACAGA	3091
Db	2933	TGAGAACATCTCTTAAAAAAGCTCAAGAGATTTGACCTGCAGGTTGACAAAGAAAGACAGA	2992
QY	3092	AGCTGAAGAGGCGATGAAGAGACATCTCTATCAGCAGAAAGGTTTCAAGGTCAGCACTGA	3151
Db	2993	AGCTGAAGAGGCGATGAAGAGACATCTCTATCAGCAGAAAGGTTTCAAGTGTCCATGCA	3052
QY	3152	CAAGACGAAGCAGACAGAAAGCAGCCCTGGGAGTGTCTGTCCGACGCCACAGAGGGGAAA	3211
Db	3053	CAAGACCCAGCAACAGAAAGAGCCCTGGGAGGCGCTGTCTGATGCACAGAGGGGAAA	3112
QY	3212	GAATGACGCCAGGAGAGGCCCTGGAGATCTCTGCGCAATGAAACAGAGATAGGAGGCT	3271
Db	3113	GAATGAGGCGCGGAGAGGCCCTGGAAATCTCCAGTGAATGTAACAGAGATTTGGAGATCT	3172
QY	3272	GAATCTGGAAACCCATGTGACAGAGATGAGCCCTTGCCCATGAGAGAGGAGTCTGGCCAC	3331
Db	3173	GAATCTGGAAACCCATGTGACAGCAGATGAGCCCTTGCCCATGAGAAAGGAGTCTGGCCAC	3232
QY	3332	TCTGAAAAAGTGAATGAGAGAAAGTGGAAGAGAGCTGTCAAGGAAGACAGAGATTGA	3391
Db	3233	TCTGAAAGTGAATGAGAGAAAGTGGAAGAGAGCTGTCAAGGAAGAGTCTGGAGTTGA	3292
QY	3392	CATGAGATTGGACAGCAGTGCAGATGATGTAATGACAGAGGCCCAAGAGAGTTGAAACAGAGC	3451
Db	3293	CACGAAATTGATGTGACAGTACAGATGTGTATTACAGAAAGCCCAAGAAAGTTGATACCAAGC	3352
QY	3452	CAAGAAATGCTGAAGTTACGATCCAAAGACACACTCAACACATTTGGATGGCATCTACACT	3511
Db	3353	CAAGAAACCTGGGTTACAAATCCAAAGACACACTCAACACATTTAAGCGCCCTCCGCACT	3412
QY	3512	AATGAGCCAGCCTGGACGCTGTGTAAGAAAGAGGCTATCTTACTGGAGCAAGACCTTT	3571
Db	3413	GATGAGCCAGCCTCTCAAGTGTGATGAAGAGAGGCGTGTCTTACTGGAGCAAGAGCTTTC	3472
QY	3572	CCGAGGCCAAGACTCAGATCAACAGCAGCAGCTACGGCCCTTGATGTCAAGAGCTGAAGAGAG	3631
Db	3473	CCGAGGCCAAGACCCAGATCAACAGCAGCACTCGGGCCATGTGTCAAGAGCTGAAGAGAG	3532
QY	3632	GGCAGATGGCAGAAAGGCGCACCTTCGTTCTCTGGAAGCTAGCATAGATGGGATTTCTGGC	3691
Db	3533	GGCAGAGTGAAGAGGGGCGCACCTTCATTTCTCTGGAAGCAAGCATAGATGGGATTTCTGGC	3592
QY	3692	TGATGTGAAGAACTCGGAGAACATCAGGGAACAACCTGGCCCCAGAGCTGTACAAATACCCA	3751
Db	3593	TGATGTGAAGAACTTGGAGAAACATTAGGGAACAACCTGGCCCCAGAGCTGTACAAATACCCA	3652
QY	3752	GGCTCTTGAGCAACAGTAGAGCTGCCTTGAAGATTTCTCAACCAAGGTTCTTGGAGATCA	3811
Db	3653	GGCTCTTGAGCAACAGTAGAGCTGCATTAATTAATTTCTCAACAGGTTCTTGGAGATCA	3712

QY 3812 GACCTAGCTGCTTAGAGATTCTCA 3837
Db 3713 GATCTCAGGGCTCGGAGCCATGTCA 3738

RESULT 4
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; Sequence 130, Application US/09466396A
; Publication No. US20030119763A1
; GENERAL INFORMATION:
; APPLICANT: Many, Tonglong
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.45504
; CURRENT APPLICATION NUMBER: US/09/466.396A
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 130
; LENGTH: 5156
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-466-396A-130

Query Match 74.1%; Score 2956.4; DB 9; Length 5156;
Best Local Similarity 88.4%; Pred. No. 0;
Matches 3285; Conservative 0; Mismatches 401; Indels 28; Gaps 6;

QY 146 CGAGGGCCGGGAGCGACCCCTGACGGGCG-----GACGGCGCGGGGCTGGCCA 198
Db 7 CGAGGGCCGGGAGCGACCCCTGACGGGAGACAGACTGAGCGCGCGCGCGCA 66

QY 199 TGCGTGGCTCTGGCTGAGCTGCTACCTGCTTCGCTTCCTGCTCCCGACCGCGG 258
Db 67 TGCGTGGCTCTGGCTGAGCTGCTGCTGCTTCGCTTCGCTTCGCTCCCGACCGCGG 126

QY 259 CCACCTCCGGGAGGAGTGTGATTTGCAAGCGGAGTCCAGCAATGCTTTGACC 318
Db 127 CCACCTCCAGGAGGAGTGTGATTTGCAATGAGGAGTCCAGCAATGCTTTGATC 186

QY 319 AGGAATTCACAAACAGACAGAAATGATTCGCTCCCTCACTGCAATGACAACTG 378
Db 187 GGGAACTTCACAGACAACTGTAATGATTCGCTCCCTCACTGCAATGACAACTG 246

QY 379 ATGGCATTCACAGAGAGTGTGATTTGCAAGCGGAGTTCACAGAGAGAAAGGACGCT 438
Db 247 ATGGCATTCACAGAGAGTGTGATTTGCAAGCGGAGTTCACAGAGAAAGGACGCT 306

QY 439 GTTTACCTGCAATTTGTAATCTTAAGGTTCTCTAGCGCTGATGACAACTGAGAC 498
Db 307 GTTTGCTGCAATTTGTAATCTTAAGGTTCTCTAGCGCTGATGACAACTGAGAC 366

QY 499 GGTGACAGCTGTAAGCCAGTGTGACAGAGAGAGTGTGACAGTGTGCTCCGGGCTCC 558
Db 367 GGTGACAGCTTAAACAGTGTGACAGAGAGAGTGTGACAGTGTGCTCCGGGCTCC 426

QY 559 ACACTACTGATGCTGGGTGCGCCCAAGACCAAAAGGCTGTAAGTCCAACTGTAAGT 618
Db 427 ACATGCTCAGAGATGGGGGTGACACCAAGAGAGTGTGTAAGTCCAACTGTAAGT 486

QY 619 GTGACACAGCTGGCATCTCAGGGCCCTGTGACTCAGGCGCTGTGTGCAAGCGGCTG 678
Db 487 GTGACACAGCTGGCATCTCAGGGCCCTGTGACTCAGGCGCTGTGTGCAAGCGGCTG 546

QY 679 TCACGTGAGAGCGCTGATAGGTGTGACAGAGTGTGTAATCACTGCACTGGATGGGGAAC 728
Db 547 TCACGTGAGAGCGCTGATAGGTGTGACAGAGTGTGTAATCACTGCACTGGATGGGGAAC 606

QY 739 CTCAGGAGCTGTACCAAGTGTGTTTGTATGGGATTCGCGACGCTGCAAGCTGAGG 798
Db 607 CTCAGGAGCTGTACCAAGTGTGTTTGTATGGGATTCGCGACGCTGCAAGCTGAGG 666

QY 799 ACTACAGTGTCCATTAATATCATCTGTGCTTCATCAAGATGTTGATGGCTGGAAGGCTG 858

Db 667 AATACAGTGTCCATTAATATCATCTGTGCTTCATCAAGATGTTGATGGCTGGAAGGCTG 726

QY 859 TCCAAAGAAAGGAGTGTGCTGCAAGGTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGG 918

Db 727 TCCAAAGAAAGGAGTGTGCTGCAAGGTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGG 786

QY 919 GCTCAGCAGCAGCAGTCAAGACCTGTCTATTTTGTAGCTCCGTGCAAAATTTCTTGGGAATC 978

Db 787 GCTCAGCAGCAGCAGTCAAGACCTGTCTATTTTGTAGCTCCGTGCAAAATTTCTTGGGAATC 846

QY 979 AAGAGTGTGAGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1038

Db 847 AAGAGTGTGAGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 906

QY 1039 ACCCATCTGCGCCATGAGAGTGTGCTGGAAGGTGCTGATGCTGACAGATCAGAGCTCCCTGA 1098

Db 907 ACCCATCTGCGCCATGAGAGTGTGCTGGAAGGTGCTGATGCTGACAGATCAGAGCTCCCTGA 966

QY 1099 TGCCACTGTGCAAGACAGTGTGCTGGAAGGTGCTGATGCTGACAGATCAGAGCTCCCTGA 1158

Db 967 TGCCACTGTGCAAGACAGTGTGCTGGAAGGTGCTGATGCTGACAGATCAGAGCTCCCTGA 1026

QY 1159 AACATCCAGCAGTAAATTTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1218

Db 1027 AACATCCAGCAGTAAATTTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1086

QY 1219 GGAAGCTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1278

Db 1087 GGAAGCTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1146

QY 1279 ACAAGTGTGATGATTTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1338

Db 1147 ACAAGTGTGATGATTTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1206

QY 1339 AATGTATATCTGCTGTTGGGTACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1398

Db 1207 AATGTATATCTGCTGTTGGGTACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1266

QY 1399 AAAGAGATTCAGCAGCAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1458

Db 1267 AAAGAGATTCAGCAGCAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1326

QY 1459 GAGGAGCTGTGATTCAGAGCAGAGAGTGTGATTCAGAGGAGGAGGAGGAGGAGGAGG 1518

Db 1327 GAGGAGCTGTGATTCAGAGCAGAGAGTGTGATTCAGAGGAGGAGGAGGAGGAGGAGG 1384

QY 1519 CTGAGTGTGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1578

Db 1385 CTGAGTGTGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1443

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Db 1504 TGTGCAATACTGCCCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1563

QY 1699 ATTTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1758

Db 1564 ATTTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1623

QY 1759 ACAAGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1818

Db 1624 ACAAGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1683

QY 1819 AGTGTATCCAGCAACAGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1878

Db 1684 AGTGTATCCAGCAACAGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1743

QY 1879 ACCCGTTGGCTCCCAATTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1938

D	b	1744	ACCATTBGGCTCCCAACCCACAGACAAGTGTCAAGCTTGGCACTGTAAACCCATGGGCT	1803
O	y	1939	CGAGGCTGTGTGAGGTGTGAAAGTATGGCAGCTGTGTTTGCAAAGCCAGGCTTTGTGGCC	1998
D	b	1804	CAGAGCCGTGTAGATGTGCAAGTATGGCAACCTGTGTGTTGCAAACGAAATTGTGTGGCC	1863
O	y	1999	TCAGCTGTAGCATGCGGCACCTGACCAAGCTGTCCAGCTTGCTATTAATCAAGTGAAGCTTC	2058
D	b	1864	CCAACTGTGACCAATGAGAGCAATT---CAGCTGTCCAGCTTCTATAATCAAGTGAAGATTCC	1920
O	y	2059	AGATGGATTCAGTTTATGACAGAGCTCCAGATCCCGAGGCGCCATATTTCCAAAGGCTCAGG	2118
D	b	1921	AGATGGATTCAGTTTATGACAGAGCTTTCAGAAATGAGAGCCCTGATTTTCAAAGGCTCAGG	1980
O	y	2119	G-----TGGAGCAGTACCCCAACCCAGAGCTGGAAGGACAGGATGCACAGGCTGACAGG	2172
D	b	1981	GTGGTGAATGGAGTATGTACTGTATACAGAGCTGGAAAGGACAGATGCACAGGCTGACAGG	2040
O	y	2173	CCCTTCCGGACATTTCTAGAGAAAGCCAGATTTCCAAAGATGCTGTTAGATCCTTCAATC	2232
D	b	2041	CCCTTCAGGACATTTCTAGAGATGCCAGATTTCCAGAAAGGTGTCAGACAGATCCCTTGATC	2100
O	y	2233	TCGGGGTGGCCAAAGGACAGCACTCAABAAGATTAAGTACCCGGAGACCGGCTGATACCTCA	2292
D	b	2101	TCGATGTTGGCCAAAGGTGAGAGGCCAAAGAAACACTTACCAAGGCGGCTGGATGATCCTCA	2160
O	y	2293	AGATGACTGTGGAAGAAGTTCGGGGCCCTGGGCACTCAGTATCACAACCAAGTTGAGATA	2352
D	b	2161	AGATGACTGTGGAAGAAGTTCGGGGCTGTGGGAAATCAATACCAAGAACCGATTTGGGATA	2220
O	y	2353	CTGGCAGGCTCATCAGTCAGATGCGCTGAGCCCTGGAGAAAGTGAAGGCTTCCCTGCAAA	2412
D	b	2221	CTCAGAGGCTCATCAGTCAGATGAGCTGAGCCCTGGCAGAAAGTGAAGCTTCCCTTGGAAA	2280
O	y	2413	ACACCAACATTTCCCTCTTCAGAGACACTACGTGGGGGCCAAATGCGTTTAAAAGTGTGGCTC	2472
D	b	2281	ACACTTAACATTTCCCTCTTCAGACACCACACTACGTGGGGGCCAAAGGCGTTTAAAAGTGTGGCTC	2340
O	y	2473	AGGAGGCCACAGAGATTTGGCAGACAGCCATGTTCAGTACAGCCAGTAAATGAGAGCACTGG	2532
D	b	2341	AGGAGGCCACAGAGATTTAGCAGAAAGCCACGTTGAGTACAGCCAGTAAATGAGAGCACTGA	2400
O	y	2533	CAAAAGAAACCCAGAGATTTCCAAAGAGCTGATGTCACTGGTGGCGGAGGCTCTGCAGG	2592
D	b	2401	CAAGGAAACCTGAGAGACTATTCCAAACAAAGCCCTCTCACTGCTGTGCGGAAAGCCCTGCATG	2460
O	y	2593	AAGAG-----GGGGAAGCGGCGAGCCTGGACGAGCCGTGTGCTCAAAAGCTTTGTGGAA	2646
D	b	2461	AAGGAGTGTGGAAAGCGGAGCGGTAGCCCGAGCGGTGTGTGTCTCAAGGCGTTTGTGGAAA	2520
O	y	2647	AATTGCGAAATCAATTAATCTGTGGCCCGCAGAGTTGTGAGAGGAGAGCCACGCAAAACCGCA	2706
D	b	2521	AATTGCGAAATCAATTAATCTGTGGCCCGCAGAGTTGTGAGAGGAGAGCCACTAAGCGGAAA	2580
O	y	2707	TGGAAGCAGATAGGTCTTATCAGCATAGTCTCAACTTCTCAATTCGCTGTCTCAGATTTC	2766
D	b	2581	TTGAAGCAGATAGGTCTTATCAGCATAGTCTCCGCTCTCTGATTCAAGTGTCTCGGCTTC	2640
O	y	2767	AGGAGTCAATGATCACTGCTTGTGCAAGT---AGAAGCGAAGAGGCTCAGACAAAAGCTG	2823
D	b	2641	AGGAGTCAATGATCACTGCTTGTGCAAGT---AGAAGCGAAGAGGCTCAGACAAAAGCTG	2700
O	y	2824	ATTCTCTCTCAAAACCGTGTGACTTAAGCATTAATGAAAGTTTCAAGCAGCTGCAAAAGCATC	2883
D	b	2701	ATTCTCTCTCAAAACCGTGTGACTTAAGCATTAATGAAAGTTTCAAGCAGCTGCAAAAGCATC	2760
O	y	2884	TGGGAAACTGGAAGAAGAAACCCGCGACGCTCTTAACAGAAATGGAAGAATGGAGACAGA	2943
D	b	2761	TGGGAAACTGGAAGAAGAAACCCGCGACGCTCTTAACAGAAATGGAAGAATGGAGAGAGA	2820
O	y	2944	CATCAGATCAGCTGCTTCCCGGTGCGCAACTTGTCTAAAAGCAGAGCCACAGAGCACTAA	3003
D	b	2821	AATCAAGTATCACTCTTCCCGGTGCGCAACTTGTCTAAAAGCAGAGCCACAGAGCACTAA	2880

QY	3004	GTATGGCAATGCCACTTTTATGAACTTGAAACATCTTAAAGATCTCAGACGTTTG	3063
Db	2881	GTATGGCAATGCCACTTTTATGAACTTGAAACATCTTAAAGATCTCAGACGTTTG	2940
QY	3064	ACCTGCAGGTTGAGATTTAAAGACAGAGCTGAAAGGGCCATGAAAGATCTCCACCA	3123
Db	2941	ACCTGCAGGTTGAGATTTAAAGACAGAGCTGAAAGGGCCATGAAAGATCTCCACCA	3000
QY	3124	TCAGCCAGAAAGTTGACAGGTCCAGTGCACAAAGACGAAGCAAGACGACCCCTGGGCA	3183
Db	3001	TCAGCCAGAAAGTTGACAGGTCCAGTGCACAAAGACGAAGCAAGACGACCCCTGGGCA	3060
QY	3184	GTGCTGCTGCCAGACGCCACAGAGGCCAAAGATTCACGCCAGGAGGCCCTGGAGATCTCTG	3243
Db	3061	GTGCTGCTGCCAGATGCACAGAGGCCAAAGATTCACGCCAGGAGGCCCTGGAGATCTCTG	3120
QY	3244	GCAAGATTCAGACAGAGATTTAGSAGSTCGAATCTTGGAAAGCCATGTGCACAGATGGAG	3303
Db	3121	GTGAGATTTGAACAGAGATTTTGGAGATCTGAAACCTTGGAAAGCCATGTGCACAGATGGAG	3180
QY	3304	CCTTGGCCATGGAGAGGAGCTGGCCACTCTGAAAGAGTGAAGATGAGAAAGTGGAGAGAG	3363
Db	3181	CCTTGGCCATGGAGAAAGGAGCTGGCCCTCTGAAAGAGTGAAGATGAGAAAGTGGAGAGAG	3240
QY	3364	AGCTGTCAAGSAGSAGSAGSAGATTTGACATGGATTTGACGCGAGTGCAGATGTTGATTG	3423
Db	3241	AGCTGTCAAGSAGSAGSAGSAGATTTGACATGGATTTGACGCGAGTGCAGATGTTGATTG	3300
QY	3424	CAGAGGCCCAAGAGATTGAAACAGAGCCAGCAAGATTCGTGAGTTACGATCCAGACACAC	3483
Db	3301	CAGAGGCCCAAGAGATTGATACGAGCCAGCAAGATTCGTGAGTTACGATCCAGACACAC	3360
QY	3484	TCACACATTTGGATGGCAGTCCTACACCTAATAGACACAGCCCTGGCAGTGTGGATGAAGA	3543
Db	3361	TCACACATTTAGAGGCGCTCTGCATCTGATGAGACACAGCCCTGCAGTGTAGATGAAGAG	3420
QY	3544	GGCTGATCTTACTGGAGAGAAAGCTTTTCCGACGCCAAGACTCAATCAACAGCCACGTAC	3603
Db	3421	GGCTGATCTTACTGGAGAGAAAGCTTTTCCGACGCCAAGACTCAATCAACAGCCACGTAC	3480
QY	3604	GGCCCTTATCTCAGAGCTGGAAGAAGAGGCGACATCGCCAGAAAGGGCCACCTCCGTTTCC	3663
Db	3481	GGCCCTTATCTCAGAGCTGGAAGAAGAGGCGACATCGCCAGAAAGGGCCACCTCCATTTGC	3540
QY	3664	TGGAGACTAGCATAGATGGAGATTCTGCTGATGTGAAGAACCTTGGAGAACTCAGAGGACA	3723
Db	3541	TGGAGAACAGATAGATGGAGATTCTGCTGATGTGAAGAACCTTGGAGAACTTGGAGGACA	3600
QY	3724	ACCTGCCCCGGGGGCTGTCACAATCCAGGCGCTTGGAGCAACAGTGAAGCTGCGCTTGAG	3783
Db	3601	ACCTGCCCCGGGGGCTGTCACAATCCAGGCGCTTGGAGCAACAGTGAAGCTGCGCTTAAT	3660
QY	3784	ATTTCACCAAGGTTCTTGGGATTCAGACCTAGCTGCTTAGAGATTTCTCA	3837
Db	3661	ATTTCACCAAGGTTCTTGGGATTCAGACCTAGCTGCTTAGAGATTTCTCA	3714
RESULT 5			
US-09-735-705-130			
; Sequence 130, Application US/09735705			
; Patent No. US20020052329A1			
; GENERAL INFORMATION:			
; APPLICANT: Wang, Tongtong			
; APPLICANT: Fan, Liqun			
; APPLICANT: Kalos, Michael D.			
; APPLICANT: Banpur, Chaitanya S.			
; APPLICANT: Hosken, Nancy			
; APPLICANT: Fanger, Gary R.			
; APPLICANT: Li, Samuel X.			
; APPLICANT: Wang, Aijun			
; APPLICANT: Skelky, Yasir A.W.			
; APPLICANT: Henderson, Robert A.			

QY 2059 AGATGATCAGTTTATGACAGCTCCAGATCTCGAGGCCCTGATTTCCAGAGCCCTCAGG 2118
 DB 1921 AGATGATCAGTTTATGACAGCTCCAGATCTCGAGGCCCTGATTTCCAGAGCCCTCAGG 1980
 QY 2119 G-----TGAGCAGTACCCAGCAGAGCTGGAGGCGAGATGACAGGCTGAGCAGG 2172
 DB 1981 GTGTGATGAGTATGATACAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2040
 QY 2173 CCGTGGGACATTTCTGAGAGAGGCCAGATTTCCAGAGATGCTGTTAGTCCCTCATC 2232
 DB 2041 CCGTGGGACATTTCTGAGAGAGGCCAGATTTCCAGAGATGCTGTTAGTCCCTCATC 2100
 QY 2233 TCCGGGTGCGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2292
 DB 2101 TCCAGTGTGGCCAGAGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2160
 QY 2293 AGATGATGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2352
 DB 2161 AGATGATGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2220
 QY 2353 CTGGCAGGCTCATCTACAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2412
 DB 2221 CTGACAGGCTCATCTACAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2280
 QY 2413 ACACCAACATTTCTCTCTGAGAGCAGTACGTTGGGAGGAGGAGGAGGAGGAGGAGGAGG 2472
 DB 2281 ACACCAACATTTCTCTCTGAGAGCAGTACGTTGGGAGGAGGAGGAGGAGGAGGAGGAGG 2340
 QY 2473 AGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2532
 DB 2341 AGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2400
 QY 2533 CAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2592
 DB 2401 CAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2460
 QY 2593 AAGAG-----GCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2646
 DB 2461 AAGAG-----GCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2520
 QY 2647 AATTGCGAAGAACTAAATCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2706
 DB 2521 AATTGCGAAGAACTAAATCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2580
 QY 2707 TGGAGGAGATGAGTCTTATCAGATGCTCCAGCTTCAATTCCTGCTGCTGAGATTC 2766
 DB 2581 TGGAGGAGATGAGTCTTATCAGATGCTCCAGCTTCAATTCCTGCTGCTGAGATTC 2640
 QY 2767 AGGAGGATGATGATCAGTCTTGCAGGT---AGAAGGAGAGGAGGAGGAGGAGGAGGAGG 2823
 DB 2641 AGGAGGATGATGATCAGTCTTGCAGGT---AGAAGGAGAGGAGGAGGAGGAGGAGGAGG 2700
 QY 2824 ATTCTCTCTCAACCGGTGCTAAGATGATGATGATGATGATGATGATGATGATGATGATG 2883
 DB 2701 ATTCTCTCTCAACCGGTGCTAAGATGATGATGATGATGATGATGATGATGATGATGATG 2760
 QY 2884 TGGAGAACTGGAG 2943
 DB 2761 TGGAGAACTGGAG 2820
 QY 2944 CATGAGATCAGTCTTCTCCGCTGCAACCTTGTAAAGAGAGAGAGAGAGAGAGAGAGAGAG 3003
 DB 2821 CATGAGATCAGTCTTCTCCGCTGCAACCTTGTAAAGAGAGAGAGAGAGAGAGAGAGAGAG 2880
 QY 3004 GATGAGGCAATGCGCACTTTTATGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAG 3063
 DB 2881 GATGAGGCAATGCGCACTTTTATGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAG 2940
 QY 3064 ACCGCGAGGTTGGAGATGAG 3123
 DB 2941 ACCGCGAGGTTGGAGATGAG 3000

QY 3124 TCAGCCAGAGGTTTGCAGTGTCCAGTGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3183
 DB 3001 TCAGCCAGAGGTTTGCAGTGTCCAGTGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3060
 QY 3184 GTGCTGCTGCCAGAGCCAG 3243
 DB 3061 GTGCTGCTGCCAGAGCCAG 3120
 QY 3244 GCAAGATGAG 3303
 DB 3121 GTGAGATGAG 3180
 QY 3304 CTTGGCCAGTGAAG 3363
 DB 3181 CTTGGCCAGTGAAG 3240
 QY 3364 AGCTGTCAAG 3423
 DB 3241 AGCTGTCAAG 3300
 QY 3424 CAGAGGCGCAAG 3483
 DB 3301 CAGAGGCGCAAG 3260
 QY 3484 TCAACAGATGAG 3543
 DB 3361 TCAACAGATGAG 3420
 QY 3544 GCGTGTCTTACAG 3603
 DB 3421 GCGTGTCTTACAG 3480
 QY 3604 GCGCTGTGATGAG 3663
 DB 3481 GCGCTGTGATGAG 3540
 QY 3664 TGGAGACTAGATGAG 3723
 DB 3541 TGGAGACTAGATGAG 3600
 QY 3724 ACCTGCCCCGCGCTGCTACAAATCCAGAGCTCTTGAGCAACATGAGAGAGAGAGAGAG 3783
 DB 3601 ACCTGCCCCGCGCTGCTACAAATCCAGAGCTCTTGAGCAACATGAGAGAGAGAGAGAG 3660
 QY 3784 ATTCTCAACCAAGGTTCTTGGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 3837
 DB 3661 ATTCTCAACCAAGGTTCTTGGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 3714

RESULT 6
 US-09-850-716A-130
 : Sequence 130. Application US/09850716A
 : Patent No. US20020115139A1
 : GENERAL INFORMATION:
 : APPLICANT: Kalos, Michael D.
 : APPLICANT: McNeill, Patricia D.
 : APPLICANT: Retter, Marc W.
 : TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 : FILE REFERENCE: 210121.455C15
 : CURRENT FILING DATE: 2001-05-07
 : NUMBER OF SEQ ID NOS: 440
 : SOFTWARE: FastSeq for Windows Version 3.0
 : SEQ ID NO 130
 : LENGTH: 5156
 : TYPE: DNA
 : ORGANISM: Homo sapien
 US-09-850-716A-130

Query Match 74.1%; Score 2956.4; DB 10; Length 5156;
 Best Local Similarity 88.4%; Pred. No. 0;
 Matches 3285; Conservative 0; Mismatches 401; Indels 28; Gaps 6;

OY	319	AGGAACCTTCACAACAGACAGAGAAATGATTTCCGCTGCTCAACTGCATATGACAACTG	378
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OY	379	ATGGCATCTCACGCGAGAGGTGCAAGGAGGATTTTTCGCGACAGAGAAAGGAGACCGCT	438
Db	247	ATGGCATCTCACTGCGAGAGAGTGCAGAAATGGCTTTTACCGGCACAGAGAAAGGAGACCGCT	306
OY	439	GTTTAAACCTCGCAATTTGTACTCTTAAAGTTCTCTTAAAGCTCGATGTGACAACCTCTGAGAC	498
Db	307	GTTTGCCCTCGCAATTTGTACTCTCAAAGGTTCTCTTAAAGCTCGATGTGACAACCTCGAGAC	366
OY	499	GGTGAAGCTTTAAAGCCAGAGTGTGACAGAGACAGGTGTGACCAGATGTCTGCCCCGCTTCC	558
Db	367	GGTGAAGCTTTAAACCCAGAGTGTGACAGAGACCAATGTGAGACCAGATGTCTGCCCCGCTTCC	426
OY	559	ACACACTCTACTGATGTGGGTGGCCGCCCAAGACCAAAAGGCTCTGAGACTCCAAAGTGTACT	618
Db	427	ACATGCTTCAGCGGATGTGGGGGTGTGCACACCAGACAGAGACTCTGAGACTCCAAAGTGTACT	486
OY	619	GTGACCCAGCTGGCAYCTCAGGGCCCTGTGACTAGGCGCCGCTGTGTCTGCAGCCGGCTG	678
Db	487	GTGACCCAGCTGGCATTCGACGGGCCCTGTGACGGGGCCGCTGTGTCTGCAGCCAGCTG	546
OY	679	TCACGTGAGAGCGGCTGTGATGTGTGACACAGGTTTCTATACCTCGATGGAGGAGAAAC	738
Db	547	TCACGTGAGAAAGCTGTGATGTGTGATCAGTTACTATTAATCTGGATGGAGGAGAAAC	606
OY	739	CTCAGGGCTGTACCCAGTGTTTTGTCTATGAGGACATTCGCCAGCTGCGACAGCTCTGAGG	798
Db	607	CTGAGGGCTGTACCCAGTGTTTGTCTATGTGGCATTTGAGGACATTCAGCCAGCTGCGACAGCTCTGAG	666
OY	799	ACTACAGTGTCCATTAATAATCATCTCTGCTCTTCATCAAGATGTTGATGTGCTGAGAGCTG	858
Db	667	AATACAGTGTCCATTAAGATACCTCTACCTTCTATCAAGATGTTGATGTGAGGCTGAGAGCTG	726
OY	859	TCCAAAGAAAGGGGCTCTGCAAAAGCTCCAGTGTGTGCACAGCGCATGGGATATATTTA	918
Db	727	TCCAAAGAAATGGGCTCTCTCTCAAAAGCTCCCATGTGTGCACAGCGCATAGATGTGTTA	786
OY	919	GCTGAGCAGCAGATCAGACCCCTGTCTATTTTGTAGCTCTGCCAAATTTCTTGGGATTC	978
Db	787	GCTGAGCCCAACAGACTAGACCCCTGTCTATTTTGTAGCTCTGCCAAATTTCTTGGGATTC	846
OY	979	AACAGGTAGCTACGGGCGCAAGCCCTATCTTTTGTAGCTACCCGTGTGATATGGGAGAGGCAGAC	1038
Db	847	AACAGGTAGCTATGTGTCAAAAGCCCTGTCTTTTGTAGCTACCCGTGTGAGACAGAGAGAGGCAGAC	906
OY	1039	ACCATATCGCCATGACGTGTGATCTCTGGAAGGTGTGCTGTGAGATCCACAGCTCCCTTGA	1098
Db	907	ACCATATCGCCCATGATGTGATTTCTGGAAGGTGTGCTGTGAGATCCAGATCCAGCTCCCTTGA	966
OY	1099	TGCCACTTAGCAAGACACTGCTTGTGTGGATTCACCAAGACTTTACACATTCGATTAATG	1158
Db	967	TGCCACTTGGCAAGACACTGCTTGTGTGGGCTCACCAAGACTTTACACATTCGATTAATG	1026
OY	1159	AACATCCAGAGATTAATTGAGAGCCGCCAGCTAAATTAATTGATATCTGGAGGTTTACTG	1218
Db	1027	AGCATCCAGGAATTAATTGAGAGCCGCCAGCTAAATTAATTGATATCTGGAGGTTTACTG	1086
OY	1219	GGAACCTTACAGCCCTGCGGATTCGAGCTACTACGGGATATACAGTACGTAGTGTGACATTTG	1278
Db	1087	GGAATCTTACAGCCCTGCGCATTCGAGCTTAATTAATTGGAATATACGATCTGTGATCATG	1146
OY	1279	ACAACGTGACCTTATTTTACAGCCGCCCTGTTCTGTGAGGCCACAGCCGCTGTGGTTGAC	1338
Db	1147	ACAATGTGACCCCTGATTTTACAGCCGCCCTGTCTGTGAGGCCACAGCCGCTGTGGTTGAC	1206
OY	1339	AATGTGATGCTCTGTGTGTGCTTACAAGGGGCGATTTCTGCGAGATTTGTCTTCCGCTTACA	1398
Db	1207	AGTGTATATGTCTGTGTGTGTACAAAGGGGCGAATTTCTGCGAGATTTGTCTTCCGCTTACA	1266

QY	1399	AAAGAGATTCCAGCAGACTGGGACCTTTTGGCACCCTGATTTTCCATGTAACCTGGCAAGGGG	1450
Db	1267	AGAGAGATTCCAGCAGACTGGGACCTTTTGGCACCCTGATTTTCTGTAACCTGCAAGGGG	1326
QY	1459	GAGGAGCCTGGGATCCAGACACAGAGACTGTTTACTAGGGGATGAGAACCTTGACATCC	1518
Db	1327	GAGGAGCCTGGGATCCAGACACAGAGACTGTTTATTCAGGGGATGAGAACTTCGACAT--	1384
QY	1519	CTGAGTGTGTGATCTGCCCATTTGGTTTCTTCAACAGATCCACAAAGACCCCGCAGCTGCA	1578
Db	1385	-TGAGTGTGTGATCTGCCCATTTGGTTTCTTCAACAGATCCGACAGACCCCGCAGCTGCA	1443
QY	1579	AGCGTGCCCTGTGTCGAATGGTTCAGCTCTCCGTGATAGCTCGAGACAGAGAGGTGG	1638
Db	1444	AGCATGTCCCTGTGTCATTAACGGGTTTCAAGCTGTCAGTGATGCCGGAACGGAGAGGTGG	1503
QY	1639	TGTGCATTAACCTGCCCCAGGGGTCTACGTGTGCCCTGTGAGCTGTGTGTGATGGCT	1698
Db	1504	TGTGCATTAACCTGCCCTTCCGGGGTCTACCGGTGCCCTGTGAGCTGTGTGTGATGGCT	1563
QY	1699	ATTTTGGGGAGCCCTTGGGGAGAGGTGGCCAGTGAAGGCCCTGTACACCCCTGTACAGTGA	1758
Db	1564	ACTTTGGGGAGCCCTTTGTGTGATGATGGCCAGTGAAGGCCCTTTGTACACCCTGTTCATGCA	1623
QY	1759	ACAACAAAGTGGACCTTGTGCTCCGGGAACTGTGACCGCTGTACAGCGCAGGTGTCTGA	1818
Db	1624	ACAACAAAGTGGACCCCGCTGCTCTGTGGAAATTTGTACCGGCTGTACAGCGCAGGTGTGA	1683
QY	1819	AGTGATTCACAACAACAGCTGGGGTCCACGTGTGACAGTGCAAAGAGGCTACTATAGGGG	1878
Db	1684	AGTGATTCACAACAACAGCGGGCATCTTATCTGTGCAACAGTGCAAAGAGGCTACTTGGGG	1743
QY	1879	ACCCTTGGGCTCCCAATCCAGACACAACAAGTGTGAGCTTGCAACTGTCAACCCAGTGGGCT	1938
Db	1744	ACCATTTGGCTCCCAACCCAGACACAACAAGTGTGAGCTTGCAACTGTCAACCCATGGGCT	1803
QY	1939	CGGAGCTGTGGAGTGTGGAAGTATGGCAGCTGTGTTTGCAAGCCAGGCTTTGTGTGGCC	1998
Db	1804	CAGAGCCCTGTGGAGTGTGGAAGTATGGCAGCTGTGTTTGCAAGCCAGGATTTGTGTGGCC	1863
QY	1999	TCAGCTGTGACATAGCGGCACTGTGACAGAGCTGCAGCTTCTATTAATCAAGTGAAGTTC	2058
Db	1864	CCAAGTGTGACATAGGACATTT---CAGCTGTCCAGCTTCTATTAATCAAGTGAAGTTC	1920
QY	2059	AGATGATCACTTTATGACAGCAGCTCCAGATCTGTGAGGCCCTGTATTTCCAAAGGCTCAGG	2118
Db	1921	AGATGATCACTTTATGACAGCAGCTTCCAGAAATGAGGGCCCTGTATTTCCAAAGGCTCAGG	1980
QY	2119	G-----TGAGAGCAATACCCAAAGCAGAGCTGGGAAGGCAGAGATGCACAGGCTGAGCAGG	2172
Db	1981	GTGGTGAATGAGTGTGTACTGTGATACAGAGGCTGGGAAGGCAGAGATGCACAGGCTGAGCAGG	2040
QY	2173	CCCTTCGGGCAATTCGTGAGAGAACCCAGATTTTACAAAGATGCTGTAGATCCCTTCATC	2232
Db	2041	CCCTTCAGAGCAATTCGTGAGAGATCCCAAGATTTTACAAAGGAGTGAAGCATCCCTTGGTC	2100
QY	2233	TCCGGGTGGCCAAAGCAGAGCACTAAAGAAATACTACCGGGAGCCGCTGGATGACTCA	2292
Db	2101	TTCCAGTTGGTCCAAAGGTGAGGACCAAGAAACACTTCCACAGAGCCGCTGGATGACTCA	2160
QY	2293	AGATGACTGTGGAAGAAGTTGGGGCCTGTGGGCAGTCAAGTATCAACAAACAGTTCAGGATA	2352
Db	2161	AGATGACTGTGGAAGAAGTTGGGGCTTGTGGAACTCAAGTATCAACAAACCGAGTTCAGGATA	2220
QY	2353	CTCGAGGCTCATCTAGATAGATGGCCCTGAGACCTGGAAGAAAGTGAAGCTTCCCTGCATA	2412
Db	2221	CTCAGAGGCTCATCTAGATAGATGAGCTGAGACCTTGGCAGAAAGTGAAGCTTCCCTGGGAA	2280
QY	2413	ACACGACATTTCTCTTCAGAGACATTAAGTGGGGCCAAATGGCTTTAAAAGTCTGGCTC	2472
Db	2281	ACATTAACATTTCTCTCTCAGACATTAAGTGGGGCCAAATGGCTTTAAAAGTCTGGCTC	2340
QY	2473	AGGAGGCCAGAGATTGGCAGACAGGCAATGTTCAAGTGAAGCAGTAAATGAGGACATGTGG	2532

||||| 2341 AGGAGGCGACAAAGTTTGTGAGAAAGCCACGTTGAGTACAGCATGAGCAACTGA 2400
2533 CAAAGAAACCCAGAGATATTCAGAGAGCTGATGATCTGTCGCGGAGGCTCTGACAG 2592
2401 CAAGGGAACCTGAGACTATTCAGAAACCCCTCTACTGTGTGCGAAGGCGCTGTATG 2460
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2461 AAGAGCTCGAAGCGGAGGAGCGGTATGCGCGAGGCTGTGTGTGTCAGAGGCTTGTGAAA 2520
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2707 TGGAGAGAGATAGTCTTATCAGATAGTCTCCACCTTCTCAATTCCTGTCTCAAGTTC 2766
2581 TTGAGAGAGATAGTCTTATCAGATAGTCTCCGCTCTGAGATTCAGTCTGTGCGCTTC 2640
2767 AGGAGTCAATGATCAGTCTCTGCAAGT---AGAGGCAAGAGGCTCAGACAAAGCTG 2823
2641 AGGAGTCAATGATCAGTCTCTCTTATAGTGTGAGAGAGCAAGAGATCAACAAAGCGG 2700
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2701 ATTCTCTCAAGCTGTGTAACAGCATATGATGATTCAAGCAGTGTCAAGCAAGATC 2760
2884 TGGGAACTGGGAAAGAAAGAAACCCGCGAGCTCTTACAGATGGAAGAAATGGGAGACA 2943
2761 TGGGAACTGGGAAAGAAAGCAAGCAAGCTCTTACAGATGGAAGAAATGGGAGACA 2820
2944 CATGAGATCAGTCTCTTCCGCTGTGCAACCTTGTAAAGCAGAGCCCAAGAACACTAA 3003
2821 AATGAGATCAGTCTCTTCCGCTGTGCAACCTTGTAAAGCAGAGCCCAAGAACACTAA 2880
3004 GTATGGCAATGCCACTTTTATGAGTTGAGAACTCTTAAAGATCTCAGAGATTG 3063
2881 GTATGGCAATGCCACTTTTATGAGTTGAGATGAGATCTTAAAGATCTCAGAGATTG 2940
3064 ACCTGCAAGTTGGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3123
2941 ACCTGCAAGTTGGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3000
3124 TCACCCAGAGAGTTGAGAGTGCAGAGTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3183
3001 TCAGCCAGAGAGTTTCAAGATGCCAGTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3060
3184 GTGCTGTGCGAGCGCCAGAGGCAAGAAATGAGAGAGAGAGAGAGAGAGAGAGAGAG 3243
3061 GCGCTGTGCTGATGCAGAGAGGCAAGAAATGAGAGAGAGAGAGAGAGAGAGAGAGAG 3120
3244 GCAAGATTAAG 3303
3121 GTGAGATTGAACAGAGATTTGGAGTTGGAATGGAAGCCAAATGTGCACACAAATGGAG 3180
3304 CCTTGGCCATGAG 3363
3181 CCTTGGCCATGAG 3240
3364 AGCTGTCAAG 3423
3441 AGCTGTCAAG 3400
3424 CAGAGGCGCCAAAG 3483
3301 CAGAGGCGCCAAAG 3360
3484 TCACACATTTGATGAG 3543
3361 TCACACATTTGATGAG 3420
3544 GCGTGTCTTACTGAG 3603
|||||

Db 3421 GCGTGTCTTACTGAG 3480
Qy 3604 GCGCTGTATGTGAGAGTGGAG 3663
Db 3481 GCGCTGTATGTGAGAGTGGAG 3540
Qy 3664 TGGAGACTAGATAGATGAGAGATTTGCTGCTGATGAGAGAGAGAGAGAGAGAGAGAGAG 3723
Db 3541 TGGAGAGAGAGATGAGAGATTTGCTGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 3600
Qy 3724 ACCTGCCCCGCGGCTGCTACATACCCAGGCTCTTGAGCAACAGTAGAGTGCCTTAGAG 3783
Db 3601 ACCTGCCCCGCGGCTGCTACATACCCAGGCTCTTGAGCAACAGTAGAGTGCCTTAGAG 3660
Qy 3784 AATTCTCAACAGAGTCTTGGATTTGAGAGTACAGTCTGCTTGAAGTTTCTCA 3837
Db 3661 AATTCTCAACAGAGTCTTGGATTTGAGAGTACAGTCTGCTTGAAGTTTCTCA 3714

RESULT 8
US-10-044-090-558
: Sequence 558, Application US/10044090
: Patent No. US20020137081A1
: GENERAL INFORMATION:
: APPLICANT: Olga Bandman
: TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
: FILE REFERENCE: PA-0028 US
: CURRENT APPLICATION NUMBER: US/10/044,090
: NUMBER OF SEQ ID NOS: 850
: SOFTWARE: PERL Program
: SEQ ID NO 558
: LENGTH: 5460
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc.feature
: OTHER INFORMATION: Incyte ID No. US20020137081A1 149791.5
US-10-044-090-558

Query Match 73.9%; Score 2949.8; DB 12; Length 5460;
Best Local Similarity 88.6%; Pred. No. 0;
Matches 3318; Conservative 0; Mismatches 392; Indels 33; Gaps 10;

Qy 99 AAGGAAAG 158
Db 14 AAGGAAAG 71
Qy 159 AGCGACCCCTGACAGCGCG-----GACCGCGCGCGCGCTGCGATGCTGCTGCTG 211
Db 72 AGCGACCCCTGACAGCGCGAG 131
Qy 212 GCTGAGCTGCTACTGCTGCTTCTGCTCTCTGCTCTGCGAGCGCGGCGACCTCTCGGAG 271
Db 132 GCTGAGCTGCTACTGCTGCTTCTGCTCTCTGCTCTGCGAGCGCGGCGACCTCTCGGAG 191
Qy 272 GGAAGTCTGATGAG 331
Db 192 GGAAGTCTGATGAG 251
Qy 332 ACAGACAG 391
Db 252 ACAGACAG 311
Qy 392 CGAGAGTGCAG 451
Db 312 CGAGAGTGCAG 371
Qy 452 TTGTAAGTCTTAAAGTCTTAAAGTCTTAAAGTCTTAAAGTCTTAAAGTCTTAAAGTCTTAA 511
Db 372 TTGTAAGTCTTAAAGTCTTAAAGTCTTAAAGTCTTAAAGTCTTAAAGTCTTAAAGTCTTAA 431
Qy 512 GCCAGGTGTGACAG 569

Db 432 ACCAGGTTGACAGGAGCCGATGGGACGATGTCTGGCCAGGCTTCCACAGCTCAGC 491
 QY 570 GATGCTGGGTCGCCCAAGACCAAGGCTGTAGACTCCAAAGTGTGACTGTGACCCAGCT 629
 Db 492 GATGGGGGGTGCACCCAGACAGCAAGAGACTGTAGACTCCAAAGTGTGACTGTGACCCAGCT 551
 QY 630 GGCATCTCAGGGCCCTGTGTGACTCAGGCGCTGTGTCTGCAAGCCGGCTGTACTGTGAGAG 689
 Db 552 GGCATGTGCAGGGCCCTGTGTGAGCGCGGCGCTGTGTCTGCAAGCCAGCTGTACTGTGAGAA 611
 QY 690 CGCTGTAGTAGTGTGACAGGTTACTATCACCCTGGATGGGGAAACCCCTGAGGGCTGT 749
 Db 612 CGCTGTAGTAGTGTGATCAGATAGGTTACTATATCTGGATGGGGAAACCCCTGAGGGCTGT 671
 QY 750 ACCAGTGTGTTTGTCTATGGGCAATTCGCGAGCTGCGACAGCTCTGAGGAGTCAAGTGTG 809
 Db 672 ACCAGTGTGTTTGTCTATGGGCAATTCAGGCACTGCGCGAGCTCTGAGAAATACAGTGTG 731
 QY 810 CATAAATCATCTCTGCTCTCCATCAAGATGTTGATGCTGGAAGGCTGTCCAAAGAAC 869
 Db 732 CATAAATCATCTCTGCTCTCCATCAAGATGTTGATGCTGGAAGGCTGTCCAAAGAAC 791
 QY 870 GGGTCTCTGCAAGGCTCCAGTGTGACAGCGCATCGGGATATATTTAGCTCAGACGA 929
 Db 792 GGGTCTCTGCAAGGCTCCAGTGTGACAGCGCATCAGCGCATCAGATGTTTATGCTCAGCCAA 851
 QY 930 CGATCAGACCCCTGTCTATTTTGTAGCTCTGCGCAAAATTTCTGGGATCAAGAGTGTGAGC 989
 Db 852 CGATCAGACCCCTGTCTATTTTGTAGCTCTGCGCAAAATTTCTGGGATCAAGAGTGTGAGC 911
 QY 990 TACGGGCAAGCTTATCTTTTGTAGCTACCGTGTGATGAGGAGGACAGACCCATCTGCC 1049
 Db 912 TATGTCACAGGCTGTCTGCTGTGACCTGCTGACAGAGGAGGACAGCCATCTGCC 971
 QY 1050 CATGAGTGTGCTGGAAGGCTGTGCTACAGATCAGACGCTCCCTGATGCGACATAGC 1109
 Db 972 CATGATGTGATTTGTGAAGTGTGCTGTGCTAGGATCAGACGCTCCCTGATGCGACATAGC 1031
 QY 1110 AAGACATGCTCTGTGGGATCACCAGACTTACACATTCAGATTAATGAAATCCAGC 1169
 Db 1032 AAGACATGCTCTGTGGGATCACCAGACTTACACATTCAGATTAATGAAATCCAGC 1091
 QY 1170 AGTAAATGGAGCCCCAGAGTAACTTCTGATTCGAGGTTTACTGCGGAACCTCACA 1229
 Db 1092 AATAAATGGAGCCCCAGAGTAACTTCTGATTCGAGGTTTACTGCGGAATCTCACA 1151
 QY 1230 GGCCTGCGGATCGAGCTACCTAGCGGAAATACAGTACTGGGTACATTTGCAAGCTGAC 1289
 Db 1152 GGCCTGCGGATCGAGCTACCTAGCGGAAATACAGTACTGGGTACATTTGCAAGCTGAC 1211
 QY 1290 TTGATTTCAAGCCCGCCGCTTCTGTGAGCCCAAGCCGCTGGTGAACATGTGTATGC 1349
 Db 1212 CTGATTTCAAGCCCGCCGCTTCTGTGAGCCCAAGCCGCTGGTGAACATGTGTATGC 1271
 QY 1350 CCTGTGGCTACAAAGGGCAGTTCTGCGAGATTTGCTCCGGCTACAAAGAGATTCA 1409
 Db 1272 CCTGTGGCTACAAAGGGCAGTTCTGCGAGATTTGCTCCGGCTACAAAGAGATTCA 1331
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 Db 1332 GCGAGCTGGGACCTTTTGGCACCTGATTCATGTAAGTCCCAAGGGGAGGGGCGCTGC 1391
 QY 1470 GATCCAGACAGAGACTGTTACTCAGGGGATGAGAACCTTGCATCTCCGTGATGTGCT 1529
 Db 1392 GATCCAGACAGAGACTGTTACTCAGGGGATGAGAACCTTGCATCTCCGTGATGTGCT 1448
 QY 1530 GACTGCCCATGCTGTTCTACAAAGATCCAGAGCCCGGAGCTGTCAAAGCCGTGCC 1589
 Db 1449 GACTGCCCATGCTGTTCTACAAAGATCCAGAGCCCGGAGCTGTCAAAGCCATGTGCC 1508
 QY 1590 TGTCCGAATGGGTGAGTGTGCTCCGTGATGCTGAGACAGAGAGTGTGTGATTAAC 1649

Db 1509 TGTCAATACGGGTTCAAGCTGTCTCAGTGAATCCGAGACGAGAGAGGTGTGTCAATTAAC 1568
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 Db 1569 TGCCCCCAGAGGTTCTACTGTGTGCCCGCTGTGAGCTGTGTGATGGATATTTTGGGAC 1628
 QY 1710 CCTTGGGGGAGCTGGGCCAGTGTGAGGCTTGTGAGCCCTGTGATGTCACAAACAACTGTG 1769
 Db 1629 CCTTGGGGGAGCTGGGCCAGTGTGAGGCTTGTGAGCCCTGTGATGTCACAAACAACTGTG 1688
 QY 1770 GACCTAGTGGCTCCCGGAACTGTGACCGCTGTGACAGGAGGCTGTGAAAGTCAATCCAC 1829
 Db 1689 GACCTAGTGGCTCCCGGAACTGTGACCGCTGTGACAGGAGGCTGTGAAAGTCAATCCAC 1748
 QY 1830 AACACAGTGGGGTCCACTGTGTGACAGTGTGCAAGAGGCTTACTATGGGACCCGTTGGCT 1889
 Db 1749 AACACAGGCGGATCTTACTGTGACAGTGTGCAAGAGGCTTACTTGGGAGCCCATTTGGCT 1808
 QY 1890 CCCAATCCAGACACAGTGTGAGGCTGTGAACTGCAACCCAGTGGGCTGTGAGGCTGTG 1949
 Db 1809 CCCAATCCAGACACAGTGTGAGGCTGTGAACTGCAACCCAGTGGGCTGTGAGGCTGTG 1868
 QY 1950 GAGTGTGAAAGTGTGAGGCTGTGTTGCAAGCCAGGCTTGTGGGCTCAGCTGTGAG 2009
 Db 1869 GAGTGTGAAAGTGTGAGGCTGTGTTGCAAGCCAGGATTTGTGGCCCAACTGTGAG 1928
 QY 2010 CATCGGCACTGACAGCTGTCCAGCTTGTCTATATCAAGTGAAGGTTCAAGATGATCAG 2069
 Db 1929 CATGAGACAT---CAGCTGTCCAGCTTGTCTATATCAAGTGAAGTGAAGTGAAGTGAAG 1985
 QY 2070 TTTATGACAGAGCTCCAGATCTGTGAGGCTGTATTTCCAGGCTCAAGG---TGGA 2123
 Db 1986 TTTATGACAGAGCTCCAGATCTGTGAGGCTGTATTTCCAGGCTCAAGGCTGTGATGGA 2045
 QY 2124 GCATGCCCAAGCAGAGCTGTGGAAGGAGGATCAGAGGCTGTGAGGAGGCTTCCGAGC 2183
 Db 2046 GTATGCTGATATCAAGCTGTGGAAGGAGGATCAGAGGCTGTGAGGAGGCTTCCGAGC 2105
 QY 2184 ATTCTGAGAGAACCCAGATTTTCAGAGATGCTGTATCTTCAATCTCCGGTGTGCC 2243
 Db 2106 ATTCTGAGAGATCCAGATTTTCAGAGATGCTGTATCTTCAATCTCCGGTGTGCC 2165
 QY 2244 AAGGCAAGACTCAAGAGATTAAGTACCGGAGCCGCTGTGATACCTCAAGATGACTGTG 2303
 Db 2166 AAGGCAAGACTCAAGAGATTAAGTACCGGAGCCGCTGTGATACCTCAAGATGACTGTG 2225
 QY 2304 GAAAGAGTTCGGGCTGTGGAGGAGTGTGACAGATTAAGTACCGGAGCTTCCGAGC 2363
 Db 2226 GAAAGAGTTCGGGCTGTGGAGGAGTGTGACAGATTAAGTACCGGAGCTTCCGAGC 2285
 QY 2364 ATCACTCAGATGCGCTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGT 2423
 Db 2286 ATCACTCAGATGCGCTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGT 2345
 QY 2424 CCTCTTCAAGAGACTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGT 2483
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 QY 2484 AGATGGACAGACGCTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGT 2543
 Db 2406 AGATGGACAGACGCTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGT 2465
 QY 2544 CAGAGTATTTCCAAAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2598
 Db 2466 GAGGACTATTTCCAAAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 2525
 QY 2599 -GCGAAGGCGGAGCTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGT 2657
 Db 2526 AGCGGAAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGT 2585
 QY 2658 ACTAAATCTGTGGCCAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGT 2717
 Db 2586 ACCAGTCCCTGTGGCCAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGT 2645

[illegible]

Dp	1032	GACACTGCCTGTGGGCTCACCAAGACTTACACATTCAGGTTAATAGAGATCCAAACAA	1091
Qy	1172	TAATGGAGCCCCCGACTAAGTAACTTGATATACGGAGTTACTGGGAACCTCAGAC	1231
Dp	1092	TAATTTGAGCCCCCGAGTGAATCTTGTGATATCGAAGGTTACTGGGAATCTCAGC	1151
Qy	1232	CTGTGGAGTCCGAGCTACCTACGAGAAATACAGTACTGGGTACATTCAGCTGACCTT	1291
Dp	1152	CCTCCGCAATCCGAGCTACATATATGGAGAAATACAGTACTGGGTACATTCAGTACCT	1211
Qy	1292	GATTTTCAGCCCGCCCGTTCTGTGAGCCCCAGCCCGCTGGGTTGAACATGTATGCC	1351
Dp	1212	GATTTTCAGCCCGCCCGTTCTGTGAGCCCCAGCCCGCTGGGTTGAACATGTATGTGCC	1271
Qy	1332	TGTTGGCTACAAAGGGGAGTTCTGCGAAGATTTGCTCCGGGTACAAAGAGATTCAGC	1411
Dp	1272	TGTTGGGTACAAAGGGGCAATTTCTGCAGAGATTTGCTTCTGGCTACAAAGAGATTCAGC	1331
Qy	1412	CAGACTGGGACCTTTTGGACACTGTATTCATGTACCTGCCAAGGGGAGGGGCTCTCGA	1471
Dp	1332	GAGACTGGGGGCTTTTGGACACTGTATTCATGTACCTGTACAGGGGAGGGGCTCTCGA	1391
Qy	1472	TCACAGACACAGAGACTGTACTCAGGGGATGAGAACCTGCACATCCCTAGTGTGTGA	1531
Dp	1392	TCACAGACACAGAGACTGTATTTATTCAGGGGATGAGAAATCTGCACAT---TGAGTGTGTGA	1448
Qy	1532	CTGCCCAATTTGGTTTCTACAAACGATCCCAAGACCCCCCGACGTGCAGAACCCCTGTG	1591
Dp	1449	CTGCCCAATTTGGTTTCTACAAACGATCCCAAGACCCCCCGACGTGCAGAACCTGTCTGTG	1508
Qy	1592	TCGCATATGGTTACAGCTCTCCGATGACCTGAGACAGAGAGAGTGTGTGCATTAAGT	1651
Dp	1509	TCATTAACGGGTTACAGCTCTCAGTGATTTCCGGAACCGAGAGAGTGTGTGCATTAAGT	1568
Qy	1652	CCCCAGGGTCTACATGTGTGCCCGCTGTGAGCTCTGTGTGATGCTAATTTTGGGGACCC	1711
Dp	1569	CCCTCCCGGGGTACACGGGTGCCCGCTGTGAGCTCTGTGTGATGCTAATTTTGGGGACCC	1628
Qy	1712	CTTGGGGGAGAGTGGCCCGAGTGAAGGCTTTGACACCCGTGATGAGCAACAAACAGTGA	1771
Dp	1629	CTTGGGTAAACATGGCCCGAGTGAAGGCTTTGACACCCGTGATTAATGCAACAAATGGA	1688
Qy	1772	CCCTAGTGCCTCCGGGAAGTGTGACCCGCTACAGGAGAGTGTGAAAGTGCATCCACAA	1831
Dp	1689	CCCGAGTGCCTCTGGGAATTTGTGACCCGGCTACAGGAGAGTGTGAAAGTGCATCCACAA	1748
Qy	1832	CACAGCTGGGCTCCACTGTGACAGTGCAGAGGCTACTATGAGGAGCCGTTGGCTCC	1891
Dp	1749	CACAGCCGGCATTTACTTCGACAGTGCAGAGGCTACTTCGGGAGCCCATTTGGCTCC	1808
Qy	1892	CAATTCAGACAAAGTGTGAGCTTGCATCTGCAATCCGACCCAGTGGGCTCCGAGCCGTGGA	1951
Dp	1809	CAATTCAGACAAAGTGTGAGCTTGCATCTGCAATCCGACCCATGGGCTCCGAGCCGTGAGG	1868
Qy	1952	GTGTGCAAGTATGGAGCTGTGTTTGCAGCCAGGCTTGTGGTGCCTCAGCTGTGAGCA	2011
Dp	1869	ATGTGCAAGTATGGAGCTGTGTTTGCAGCCAGATTTGTGGCCCAACATGTGAGCA	1928
Qy	2012	TGCGGCACTGACAGCTGTCCAGCTTGCATATATCAAGTGAAGGTTCAGATGATCAGTT	2071
Dp	1929	TGAGGCAAT---CAGCTGTCCAGGCTGCTAATAATCAAGTGAAGTTCAGATGATCAGTT	1985
Qy	2072	TATGCAAGAGTCCAGATCTCTGGAGGCCCTGATTTTCCAGAGGCTCAGG-----TGAGC	2125
Dp	1986	TATGCAAGAGTTCAGAAATGAGAGGCCCTGATTTTCAAAGGCTCAGGCTGATGATGAGT	2045
Qy	2126	AGTACCCAGCAGAGCTGGAAGGACAGATTCAGACAGCTGAGCAGCCCTTCGGAGAT	2185
Dp	2046	AGTACCTGATACAGAGCTGGAAGGACAGATTCAGACAGCTGAGCAGCCCTTCGGAGAT	2105
Qy	2186	TCTGAGAGAACCCAGATTTTCAAGATGCTGTAGATCTTCAATCTCCGGGTGGCAA	2245

Db	2106	TCGTGAGAGATGGCCAGATTTTCAGAAAGGTGCTAGACGATCCCTTGCTCCAGTTGGGCCAA	2165
QY	2246	GGCAGGACACTCAGAGAAATAGCTACCGGGACCCGCTGGATGACCTCAAGATGACTGTGA	2305
Db	2166	GGTGTAGAGGCCAAGAGAAACAGACTACCGAGACCAGCGCTGGAGACTCAAGATGTACTGTGA	2225
QY	2306	AAGAGTTCGGGGCCCTGGGGCAGTCAAGTATCCAGAACCAAGTTCAGATACCTGGCAGGCTCAT	2365
Db	2226	AAGAGTTCGGGGCTCTGGGAAATCGTACCGAAGACCGAGTTCTGGGATACCTCAGAGGCTCAT	2285
QY	2366	CACACAGATGGCCCTGGAGCCCTGGAGGAAAGTGAAGGCTCCCTGGCAAAAACCAACATCTCC	2425
Db	2286	CACACAGATGAGCTGTAGCCCTGGGAGAAAGTGAAGCTCTCTTGGGAAACACTAACATCTCC	2345
QY	2426	TCCTTCAGAGCACTAGCTGGGGCCAAATGGCTTTAAAAAGTCTGGCTCAGGAGGCCACGAG	2485
Db	2346	TGCCTCAGACCACTACCTGGGGCCAAATGGCTTTAAAAAGTCTGGCTCAGGAGGCCACAG	2405
QY	2486	ATTGGCAGACAGCCATCTCAGTCAGCCAGTAACTATGGACCAACTGGCAAAAGGAAACCCA	2545
Db	2406	ATTAGCGAAGAAAGCCACCTTGATGCTAGCCAGTAACTATGGACCAACTGCAAGGGAAACTGA	2465
QY	2546	GGAGTATTTCCAAAGAGCTGATGTCACCTGTCGGGAGGAGGCTCTGCAGAGAAAGAG-----G	2599
Db	2466	GGACTATTTCCAAAGAACCCCTCTACCTGCTGCGAAGGAGCCCTGATAGAGAGTCCGAGAG	2525
QY	2600	CGGAAGCGGCAGCCCTGGACGGAGGCCGCTGTGCCAAAGGCTTGTTGGGAAATTTGCAGAAAC	2659
Db	2526	CGGAAGCGGATGCGCCGAGCGGTGCTGTGTGCCAAGGGCTTGTTGGAAATTTGCAGAAAC	2585
QY	2660	TAAATCTCTGGGCCCGAGAGTGTGTGAGGAGGAGGCCACGCCAAACGACATGGAGCAGATAG	2719
Db	2586	CAAGTCCCTGGCCCGAGAGTGTGAAGAGGAGGCCACCTCAAGCGGAAATTTGAGCAGATAG	2645
QY	2720	GTCCTTACAGATAGTGTCCACCTTCCTCAATCCCTGTCAGATTCAGGAGAGTCATGA	2779
Db	2646	GTCCTTATCAGACAGTCTCCGCTCTCTGATTCAGTGTCTTCGCTTGAGGAGAGTCAGGA	2705
QY	2780	TCAGTCCCTGGCAGGT--AGAAAGCAGAGAGGCTCAGACAAAAAAGCTGATTTCTCTCAAA	2836
Db	2706	TCAGTCCCTTCAGGTGGAAGAAAGCAAAAGAGATCAAAACAAAAGCGATTCACCTCTCAG	2765
QY	2837	CCGTGTGACTAAGACATATGATGATGATTCAGACACGTCGCAAAAGCATCTGGGAAACTGGGA	2896
Db	2766	CCTGTGTAACCGAGGATATGATGATGATTCAGACGTCACAAAAAAGATCTGGGAAACTGGAA	2825
QY	2897	AGAGAAACCCGGGAGGCTCTACAGANTGGAAGAAATATGGGAGAGACATACGATTCAGCT	2956
Db	2826	AGAAAGAACACAGACGCTTTCACGAATATGGAAGAAAGTGGGAGAGAAATACGATTCAGCT	2885
QY	2957	GCTTTCGCCGTCACAACCTTGCTAAAGCAGAGCCCAAGAAAGCACTAGTATGGGCAATGCG	3016
Db	2886	GCTTTCGCCGTCACAATCTTGCTAAAGCAGAGACCAAGAAAGCACTAGTATGGGCAATGCG	2945
QY	3017	CACTTTTTATGAGTGAAGACATCTTAAAGATCTCAGAGAGTTTGAACCTGCAGGTTGG	3076
Db	2946	CACTTTTTATGAGTGAAGACATCTTAAAAACCTCAGAGAGTTTGAACCTGCAGGTTGA	3005
QY	3077	AGATPAAAAGACACAGAGCTGAAGAGGCCATGAAGAGACTCTCCCTACATCAGCCAGAAAGT	3136
Db	3006	CAACAGAAAACACAGAGCTGAAGAGGCCATGAAGAGACTCTCCCTACATCAGCCAGAAAGT	3065
QY	3137	TGCAGAGTCCAGTGACAAAGAGAGCAAGCAGAGAGACGCTCTGGGCAAGTGTGTGTCGCGA	3196
Db	3066	TTCAGATGCCAGTGACAAAGACCCAGCAAGCAGAAAGAGCCCTGGGAGACGCTGCTGCTGA	3125
QY	3197	CGCCACAGAGGCAAGAATGCAGCCAGGAGGCGCTTGAGATCTCTGGCAAGATPAGACA	3256
Db	3126	TGCACAGAGGCGCAAGATGGGGCGGGGAGGCGCTTGAAATCTTCAGATGAGATTGAACA	3185
QY	3257	GGAGATATGGAGGTCTGAACTTGAAAGCCAAATGTACAGCAGACATGAGAGCTTGGCCATGGA	3316
Db	3186	GGAGATATGGAGGTCTGAACTTGGAAGCCAAATGTACAGCAGACATGAGAGCTTGGCCATGGA	3245

OY	3317	GAAGGACCTGGCCACTCTGGAAAAGTGGATGAGAGAAAGTGGAAAGAGAGCTGTCAAGAA	3376
Db	3246	AAAGGAGTGGCCCTCTCTGGAAGAGTGAATGAGGAAGTGGAAAGAGAGAGCTGGAAGGA	3305
OY	3377	GGACGAGAGCTTTACATGATGATATGAGAGCGACGTGCAGATGGTAATTGGCAGAGGCCCAAG	3436
Db	3306	GGACCTGGAGTTTACACGAGATATGGAATGGCATGCAGTGGTGATTTACAGAAGGCCGAA	3365
OY	3437	AGTTGAAAACAGAGCCCAAGAATGCTGGAGTTACGATCCAMGACACACTCAACACATTGGA	3486
Db	3366	GGTTGATACCGAGAGCCAAAGACGTGGGGTTACATCCAAAGCACACTCAACACATTAGA	3425
OY	3497	TGGCATCCTACACCTAATAG	3516
Db	3426	CGGCTCTCGCATCTGATGG	3445

```

RESULT 11
US-10-037-182-15
: Sequence 15, Application US/10037182
: Publication NO. US20030044899A1
: GENERAL INFORMATION:
: APPLICANT: Tiyyavason, Karl
: APPLICANT: Doi, Masayuki
: APPLICANT: Thyboll, Jill
: TITLE OF INVENTION: Recombinant Laminin 10
: FILE REFERENCE: 99-274-F
: CURRENT APPLICATION NUMBER: US/10/037,182
: CURRENT FILING DATE: 2001-12-21
: PRIOR APPLICATION NUMBER: 60/257,449
: PRIOR FILING DATE: 2000-12-21
: PRIOR APPLICATION NUMBER: 60/279,282
: PRIOR FILING DATE: 2001-03-28
: NUMBER OF SEQ ID NOS: 36
: SOFTWARE: Patentin Ver. 2.0
: SEQ ID NO 15
: LENGTH: 4948
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)..(4728)
: US-10-037-182-15

```

Query Match	12.9%	Score 515.6	DB 9	Length 4948
Best Local Similarity	58.8%	Pred. No. 1.2e-153		
Matches 978; Conservative	0	Mismatches 654	Indels 30	Gaps 4

OY	278	CTGTGATTGCACAGGGAAATCCAGGCCAATGCATCTTTTGACCAGAAGCACTTCAACAACAGAC	337
Dd	924	CTGTGATTGCACATGGTCATCGATCCAGGAATGCTACTTCGACCCOTGAACCTCTATCGTTTCCAC	983
OY	338	AGGAATAGGATTCGCGTCCCTCCTCAGCTCATGCAATGACACACATGATGGCATTCACACTGGGAAG	397
Dd	984	TGGCCATATGGGGGCCCACTCTGTACCACAACTGGCACAGGATTAACACAATATGGCGCCCACTGTGAAG	1043
OY	398	GTCGACAGCAGGATTTTACCGACAGAGAAAGGACCGCGTTTACCCTGCATTTGTA	457
Dd	1044	GTGCCGAGAGAACYCTTTCGCGCTTGGCAACATAAGAACCTGTGCTTTATGCGACTGTAG	1103
OY	458	CTCTAAAGGTTCTCTTAGCGCTGCATGTGACAACTGTGAGCGTGGACAGCTGTGAAGCCAGG	517
Dd	1104	TCTCTATGGGCTCTCTTAACACACAGTGTGATAGTAAAGGCAGATGCACACTGTAAACCCAGG	1165
OY	518	TGTGCAGAGACAGGTGACCCGATGTCTGCCCCGCTTCCACACACTCAGTATGCTGG	577
Dd	1164	AAGTATGGGGGACAATATGTGACCGTTGCCAGCCTGGATTCATCTCTCACTGGAAGCAGG	1222
OY	578	GTGCGCCCACAAAGCCAAAGGCTGCTAGACTCCAAAGTGTACTGTAGCCACAGCTGGGATCTC	637
Dd	1224	ATGCAAGGCCA-----TGTCTTGTATCCCTCTGGCAGCATAGANTGA	1265

QY 638 AGGCCCTGTGACTCAGGCCGCTGTCTGCAAGCCGGCTGTACTGAGAGCGCTGTGA 697
DB 1266 ATGTAAATGTGAAACAGAGATGCTTTGCAAGCAATGTGCAAGGCTTCAATGTGA 1325
QY 698 TAGTGTGACGACGAGTTACTATACCGATGAGTGGGGAAACCCACAGGGCTGTACCAGT 757
DB 1326 AATATGCAACGCTGAGATTTTATATGCAATCATCTAATCTCGGGGGTGTGACACCTG 1385
QY 758 TTTTCTATATTTGATTTCCGACAGTCCACAGCTGTGGGAGTACAGTGTCCATTAAT 817
DB 1386 CTTCCTGTTGGGCAATTCCTCTGTCTGTAACAAGCTGTGGGTACAGTGTATATCTAT 1445
QY 818 CATCTGTCCCTTCATCAAGATGTGATGGCTGGAAAGCTGTCCAAAGAAAGGGTCTCC 877
DB 1446 CTCTCTACCTTTCACATTTGATGATGAGTGGTGGCGGGAACAGAGATGGCTGTGA 1505
QY 878 TGCAAAGCTTCAGTGTGACAGCGCATGGGATATATTAGTCAAGCAGCATGATAGA 937
DB 1506 AGCATCTCTGAGTGTCTCTGAGAGGCAAGATATCGCGTATCTCAGACAGTACTT 1565
QY 938 CCCGTCTATTTTGTAGTCTCTGCAAAATTTCTTGGGAATCAACAGGTAGTACGGGCA 997
DB 1566 TCTCGGTACTTATTCCTCTCTGCAAAAGTCTTGGGCAAGCAGGTGTGAGTATGTCA 1625
QY 998 AAGCCTATCTTTGACTACCGTGTGATAGGGAGCAGACACCCATCTGCCATAGCT 1057
DB 1626 GAACCTCTCTCTCTCTCTGATGAGGAGGCAATCTCGCTCTGCTCCCAAGACCT 1685
QY 1058 GATCTGGAAGGTGTGCTACAGATCAAGCTCCCTGTGATCCCATTAAGCAAGACCT 1117
DB 1686 TGTGCTGAGGAGCTGTGCTTAAGATATCTGATCCCTGATGCTCAGGGCAATTCCTA 1745
QY 1118 GCTTGTGGGATCAGCAAGACTTACATTCAGATTAATTAATCAACATCCAGCATATTG 1177
DB 1746 TCCAAAGTGAACACATGTGATGATGTCTTCAAGGCTCCATGAAGCAAGATTAACCTTG 1805
QY 1178 GAGCCCCGACTAGTACTTTAGATGTGGAGTACTGCGGAACTCAGACCTGCG 1237
DB 1806 GAGGCTGTCTTACCCCTTTTGAATTTGAGAAGCTCTCAAAACCTTGAACCTCTATCA 1865
QY 1238 GATCCGAGCTACTGAGAGAAATACATGCTGCTGATGATGACAGCTGATTTTC 1297
DB 1866 GATACGTGGACATACAGTGAAGAAAGTGTGATATTTGGATGATGTCACCTGGCAAG 1925
QY 1298 AGCCGCCCCGTTTGTGAGACCCCAAGCCGCTGGGTTGAACAATGTGTATCCCTGTGG 1357
DB 1926 TGTCTCTCTGCGGCTGTGAGTCCCTCAACTTGGTGGAGTCTGTCAACCTGTCTGTGG 1985
QY 1358 CTACAGGGGCAAGTCTGCAAGATGTGCTTCCGCTACAAAAGATTCAGCCAGACT 1417
DB 1986 ATATGAGGGGCAATTTTGTGAGATGTGCTCTCAGGTTACAGAAAGAAATCTCTATCT 2045
QY 1418 GGGACCTTTTGGACCTGTATTCATGTAATGCCAAG--GGAGGGGCTGTGATCC 1474
DB 2046 TGGACATACAGTCCATGTGTGCTTGGCGCTGCATAGGACAGAGAGATCTGTATCC 2105
QY 1475 AGACACAGAGACTGTACTCAGGGATGAGAACTGTACATCCCTGAGTGTGCTAGT 1534
DB 2106 TGAAGACAGGTGTGTAACTGAGAGACAATACGCTG--GCCCCACAGTGAAGT 2162
QY 1535 CCCCATTGTTCTACAAAGATCCACAAG-----CCCCGAGTGTGCAAGCCGTGCCC 1588
DB 2163 CAGTGTGGGTACTATGAGATTCACCTCAGGCACTCTCCGATTTGCAACCCCTGTGC 2222
QY 1589 CTGTCCAAATGGGTAGCTGTCTGATGCTGTGACAGAGAGAGGTGTGCAATTA 1648
DB 2223 GTGTCTGAGAGTCAAGTGTGTCTTGTTCCTCAAGACAAAGAGAGTGTGTGCA 2282
QY 1649 GTGCCCCAGAGTGTCACTGTGCCCCGTGTGAGCTGTGTGATGAGCTATTTGGGGA 1708
DB 2283 CTGTCTACTGTGACACACTGTGAAGATGTGAGCTCTGTGATGATGGGTACTTTGGAA 2342
QY 1709 CCCCTTGGGGAACGTGGCCCAAGTGAAGCCCTTGTCAAGCCCTGTCACTGCAACAACAGCT 1768

RESULT 12
US-10-037-182-13
; Sequence 13, Application US/10037182
; Publication No. US2003004489A1
; GENERAL INFORMATION:
; APPLICANT: Trygveason, Karl
; APPLICANT: Doi, Masayuki
; APPLICANT: Thyboll, Jull
; TITLE OF INVENTION: Recombinant Lamidin 10
; FILE REFERENCE: 99-274-F
; CURRENT APPLICATION NUMBER: US/10/037,182
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,449
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/279,282
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 5306
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (260)..(5086)
; NAME/KEY: sig peptide
; LOCATION: (260)..(358)
US-10-037-182-13
Query Match 12.9%; Score 515.6; DB 9; Length 5306;
Best Local Similarity 58.8%; Pred. No. 1,2e-153;
Matches 978; Conservative 0; Mismatches 654; Indels 30; Gaps 4;
QY 278 CTGTGATTCAGGGAAGTCCAGGCAATGATCTTTGACACGAGAACTTCACAACAGAC 337
DB 1282 CTGTGATTCAGGGAAGTCCAGGCAATGATCTTTGACACGAGAACTTCACAACAGAC 1341
QY 338 AGGAAATGATTCGCTGCTCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 397
DB 1342 TGGCATTGGGGGCTGATGACACAGTCCAGGATTAACAGATGAGTGGCCACTGTGAGAG 1401
QY 398 GTGCAAGCAGAGATTTTACGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 457
DB 1402 GTGCGCAGAGACTTCTTCCGCTTGGCAACAATGAGAGCTGTCTTCAATGCCACGTGAG 1461
QY 458 CTCTAAAGTTCTCTTAGCGCTGTGATGACAACTCTGAGCGGTGACAGTGTGATGAGCAG 517
DB 1462 TCTGTGGGCTCTCTTAAGACACAGTGTGATGATGATGATGATGATGATGATGATGATG 1521
QY 518 TGTGACAGAGAGAGTGTGACAGAGTGTGCGCCGCTTCCACACACTACATGATGCTGG 577
DB 1522 AGTATGAGGGGCAAAATGTGACCGTTCAGCTGTGATTCATTTCTCTCACTGAACAGG 1581
QY 578 GTGCGCCCAAGACCAAGAGCTGTGATGACCAAGTGTGATGATGATGATGATGATGATG 637
DB 1582 ATGCAAGGCA-----TGTCTTGTGTATCCCTCTGAGCAATGATGA 1623

QY	638	AGGCGCCCTGACACGAGCCCGCTGCTGTCGACACCGCCGCTGCTACCTGAGAGCGCTGGA	697
Db	1624	ATGTAAATGTTAAACACAGAAAGATGTGTTTGCAGAAAGCAATGTCCAAAGCTTCAATTGTGA	1683
QY	698	TAGGTGTGACACAGGTTACTATACCTCGATGAGGGGAAACCCCTGAGGCTGTACCCAGTG	757
Db	1684	AAGATGCAACCTGGATTTTTTAAATCTGGAATCATCTAATCTCGGGGTTGCACACCCTG	1743
QY	758	TTTTTGCTAATGGCATTCCGCCAGCTGCCACAGCTGTGGGGAGTACAGTGTCCATAAAT	817
Db	1744	CTTCTGCTTTGGGCAATTCCTCTGCTGTACAAAGCGCTGTGGCTACAGTGTATTATCTAT	1803
QY	818	CATCTGCGCCTCCATCAAGATGTGTAGTGGGTGGAAGCGCTGCCAAGAAAGGGCTGCC	877
Db	1804	CTCTCTACCTTTTAGATTGATGAGGATGGGTGGCGTGGCAAGAGAGATGGCTCTGA	1863
QY	878	TGCMAAGCTCCAGTGTGTACAGAGCCCATCGGGAATATTTAGTCTACACAGCATCAGA	937
Db	1864	AGCATCTCTGAGTGGTCTCTGTGAGGAGCAAGATATGCCCTGATCTCAGACACTACTT	1923
QY	938	CCCTGTCTAATTTGTAGCTCTCGCCAAATTTCTTGGAAATCAACAGGTAGACTAGGGCA	997
Db	1924	TCCCTGCTACTCTCATTTGCTCCTCGCAAGATCTTGGCAAGAGAGGTGTGAATTATGTC	1983
QY	998	AAGCCTAATCTTTTACTACGCTGTGATAGGGGAGGAGACACCATTCTGCCATGACGT	1057
Db	1984	GAACTCTCTCTTCCCTTTTGGAGGAGCAGGCGGAATATCTGCTCTCTGCGGAAGACT	2043
QY	1058	GATCCTCGAAGGTCTGTGTACAGGATCACAGCTCCCTGTGATGCTACTTACCAAGACT	1117
Db	2044	TGTCTTGAGGAGACTGTGCTTAAAGATATCTGTACCTGTATCGCTCAGGGCAATTTCTTA	2103
QY	1118	GCTTTGTGGATCACCAAGACTTACACATTCAGATTAAATGAAATCCAAAGCAGTAATTG	1177
Db	2104	TCCAAAGTGAAGCCACTGTGAAGTATGTTCTCAGGCTCCATGAGCAACAGATTAACCTTG	2163
QY	1178	GAGCCCCCAGCTAAGTTACTTTGAGTATCGGAGTTACTGCGGAACCTCACAGCCCTGCG	1237
Db	2164	GAGGCTGCTCTTACCCCTTTGAAATTTCAAAACCTCTTAACAACTTGACCTCTATCA	2233
QY	1238	GATCCGAGCTACCTACGAGAGAAATACAGTACTGGGTACTATACAAAGGACCTTGATTTTC	1297
Db	2224	GATACGTGGGACATACAGTGAAGAAATGCTGGAATTTGGATATGTCTACCTGTGGCAG	2283
QY	1298	AGCCCGCCCGTTCGTGAGGCCAGCGCCCTGGGTTGAACAATGTGTATGCCCTGTGG	1357
Db	2284	TGCTGTGTCGTGGGCTGGAGTCCCTGCAACTTGGGTGAGTCTGACACCTCTCGTGGG	2343
QY	1358	CTACAAAGGGGAGTTCGACAGGATTTGTGCTCCGGCTACAAAGAGATTAGCCAGACT	1417
Db	2344	ATAATGAGGAGAGTTTGTGTGAGATGTGCTCTCAGGTTACAGAAAGAAATCTCTAATCT	2403
QY	1418	GGGACCTTTTGGACCTGTATTCATGTAACTGTGCCAAGG---GGGAGGGGCTGCGATCC	1474
Db	2404	TGGACCTATACGTCATATGTGTGCTTTTGGCGCTGGAATGACACACGAGACTGTGATCC	2463
QY	1475	AGACACAGGAGACTGTTACTACGAGGAGTGAACACCTGACATCCCTGATGTGTGATG	1534
Db	2464	TGAGACAGAGGTGTTGTAACTGTCAAGACAAATACGGGTG---GCCGACCTGTGAAGATG	2520
QY	1535	CCCCATTGTTTCTACACAGATCCACAAGA-----CCCCGCAAGCTGCAACCGGTGCC	1588
Db	2521	CAGTGAATGGGTACTATGAGAAATCAACTGACAGGACCTCTCCCATTTCCAAACCTGTGC	2580
QY	1589	CTGTGCGAATATGGGTACGCTGCTCGGTGATGCCCTGAGACAGAGAGGGTGTGCAATA	1648
Db	2581	GTGTCTGTGAGGTTCAAGTTGTGTCTGTGTTTCCAAAGCAAAAGGAGGTGTGCACCAA	2640
QY	1649	CTGCCCCCAGAGGTACATGTGTGCCGCTGTGACTGTGTCTGATATGCTATTTTGGGGA	1708
Db	2641	CTGTCTCACTGTGCAACCACTGATTAAGAAATGTGAACTGTGTATATATGCTACTTTGGAGA	2700
QY	1709	CCCCTTGGGGGAAGCTGGCCAGTGAAGGCTTTGTCAAGCCCTGTCAATGTCAACAACACTG	1768

Db	2701	CCCCCTGGTAGAAGAACGGCCCTGTGTGACACTTTGGCGGCTGTGGCAGTGTGACAGTACAT	2760
QY	1769	GGACCTTAGTGCCTCCGGGAACTGTGAACCGCTGTGACAGGAGGTGTGTGAATGCATCA	1828
Db	2761	CGATCCCAAGCAGCACTTGGAAATTTGCATTCGCTTGACGGGAAATGCTGGAAGTGCATCTA	2820
QY	1829	CANACAGCTGCGGCTCCACGTGTGACAGTGAAGGAGGAGGCTACTAGTGGGACCGGTGGC	1888
Db	2821	TAAACAGCTGCGCTTCTATTTGTGTGACCGGTGCAAGAGAGGATTTTTTGGAAATCCCTGGC	2880
QY	1889	TCCCAATCCAGACAGACAAGTGTCCAGCTTGCAATGCAGACC	1930
Db	2881	TCCCAATCCAGACAGACAATGTCAAAAGCCTGCAATTCGATCC	2922

RESULT 13

US-10-084-817-81

Sequence 81, Application US/10084817

Publication No. US20030119009A1

GENERAL INFORMATION:

APPLICANT: Susan Stuart

APPLICANT: Jed G. Nuchtern

APPLICANT: Sharon E. Plon

APPLICANT: Jason M. Shohet

TITLE OR INVENTION: GENES REGULATED BY MYCN ACTIVATION

FILE REFERENCE: PA-0046 US

CURRENT APPLICATION NUMBER: US/10/084,817

CURRENT FILING DATE: 2002-02-25

PRIOR APPLICATION NUMBER: 60/270,784

PRIOR FILING DATE: 2001-02-23

NUMBER OF SEQ ID NOS: 365

SOFTWARE: PERL Program

SEQ ID NO 81

LENGTH: 7812

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc_feature

OTHER INFORMATION: Incyte ID No. US20030119009A1 252151.12

NAME/KEY: unsure

LOCATION: 3983

LOCATION INFORMATION: a, t, c, g, or other

US-10-084-817-81

Query Match 12.9%; Score 515.6; DB 9; Length 7812;

Best Local Similarity 58.8%; Pred. No. 1,6e-153;

Matches 978; Conservative 0; Mismatches 654; Indels 30; Gaps 4;

QY	278	CTGTGATTGTCACAGGGAGATCCAGAGCATGATCTTTGACCAAGAACTTCAACAAGAC	337
Db	1282	CTGTGATTGTCATGTGTGATGTGATCCAGGAATGCTTACTTGACCCCTGAACTCTATCGTCCAC	1341
QY	338	AGGAATATGATTCCGCTGCTCACAACGTCAATGACACAACATGATGATCCACTCGAGAG	397
Db	1342	TGGCATTGGGGGCCACTGTATACCACTGCGACAGATATACACAGATGGCGCCACTGTGAGAG	1401
QY	398	GTGCAAGCAGAGATTTTACCGACAGAGAGAAAGGAGCAGCGCTTTTACCTGCATTTGAA	457
Db	1402	GTCGCGAGAGACATCTTCCGCTTGGCAACAAATGAAGCCGCTTCATGACACTGTAG	1461
QY	458	CTCTAAAGGTTCTTATAGCCCTGCATGTGACAACCTGTGAGAGGTGACAGCTTAAGCCAGG	517
Db	1462	TCTCTGTGGGCTCTTAAGCACAACAGTGTGATAGTTAAGGACAGATGTGACAGCTTAAGCCAGG	1521
QY	518	TGTGACAGAGACAGGTGTGACCGAGATGTCCCGGCTTCCACACACTCACTGATGCTGG	577
Db	1522	AGTATGAGGGGACAATATGTGACCGCTGCAACCTCGGATTCATCTCTCACTGAAGCAGG	1581
QY	578	GTGGGCCCCAACAACAAAGGCTGTAGATTCACAATGAGACGTGTGACCCAGCTGGCATCTC	637
Db	1582	ATGCAAGGCCA-----TGCTCTGTGTATCCCTCTGGCAGCATATAGTGA	1623

Db 1724 AGATGCAAACTGGATTTTATATCTGCATCATTAATCTGGGGTTGCAACCCCTG 1783
 QY 758 TTTTGTCTATGGGCAATTCGCGCAGCTGCCACACAGCTCTGGGGACTACAGTGTCCATAAAT 817
 Db 1784 CTTCCTCTTGGGCAATTCCTGTGTGTACAAAGCGTGTGGCTACAGTGTATTTCTAT 1843
 QY 818 CATCTGCTCTTCATCAAGATGTGTATGGGTGGAAGGCTGTCCAAAGAAAGGGGTCTCC 877
 Db 1844 CTCCCTTACCTTCATCAATGTATGATGATGGGTGGGCAACAGAGATGGCTCTGA 1903
 QY 878 TGCAGAGCTTCAGTGGTCAACAGCGGCATATATTAGCTTCAGCAGAGATCAGA 937
 Db 1904 AGCATCTCTGAGTGTCTCTGAGAGGCAAGATATCGCCGTGATCTCAGACGCTACTT 1963
 QY 938 CCCGTCTATTTTGTAGCTCTGCGCAATTTCTTGGGAATCAACAGGTAGCTACGGCA 997
 Db 1964 TCCTGGTACTTCATGTCTCTGCAAAAGTTCTTGGGCAAGCAGGTGTGATGTATGTCA 2023
 QY 998 AAGCCTATCTTTGACTACCGGTGTGATAGGGGAGCAGACACCCATGTGCCATGACGT 1057
 Db 2024 GAACCTCTCCTTCTCCTTCGAGTGACAGGCGAGATACCGCTCTGTGCCAGAGACCT 2083
 QY 1058 GATCCGGAAGGTGCTGCTCTGATGATCAAGCTCCCTGATGCCACTTAGCAAGACCT 1117
 Db 2084 TGTGCTTGAGGGAGCTGGCTTAAGAGTATCTGACCTTGATCTCAGGGCAATTCCTA 2143
 QY 1118 GCGTTGTGGGATCCACCAAGCTTACATTCAGATTAAATGAACATCCAAAGCAGTAAATG 1177
 Db 2144 TCCAACTGAGACCACTGTGATATGTCTTCAGGCTCCATGAAGCAACAGATTACCCCTG 2203
 QY 1178 GAGCCCCAGCTAAGTACTTGTAGATGAGAGGTTACTGCGGACCTCAGACCCCTGCG 1237
 Db 2204 GAGGCTGCTTACCCCTTTGAAATTCAGAGCTCTAAACACTGACCTCTATCAA 2263
 QY 1238 GATCCGAGCTACCTAGGAGAAATACAGTCTGGGTACATTGACAGAGTGAATTC 1297
 Db 2264 GATAGCTGGACATACAGTGAAGAGAGTCTGATATTTGGATGATGTCACCTGGCAAG 2323
 QY 1298 AGCCCGCCCGTTCTGAGAGCCCGCAGCGCTGGTGAACAATGTATGCCCTGTGG 1357
 Db 2324 TGTGCTGCTGGGCGCTGAGAGTCCCTGCAACTTGGGTGAGTCTGCACTGTCTGTGG 2383
 QY 1358 CTACAAAGGGCAGATTCTGCCAGAGATGTCTCTCCGCTACAAAGAGATTCAAGCAGACT 1417
 Db 2384 ATATGAGGGCAGATTGTGAGATGTGCTCTCAGGTTACAGAAAGAAATCTCTAATCT 2443
 QY 1418 GGGACCTTTGGACCTGATTCATGCTAATGAGCCAAAG---GGGAGGGGCTGCGATCC 1474
 Db 2444 TGGACCATACAGTCCATGTGTGCTTGGCGCTGCAATGAGACACAGCGAGACCTGTGATCC 2503
 QY 1475 AGACACAGGAGACTGTACTACAGGGATGAGAACCTGACATCCCTGAGTGTGCTGACTG 1534
 Db 2504 TGAAGAGGTGTTGTAACTGACAGACATATGCGCTG---GCCCGCACTGTGAGAGATG 2560
 QY 1535 CCCCATGTGTTCTACACGATCCACAGA-----CCCCCGAGCTGCAAGCCGTGCC 1588
 Db 2561 CAGTGTGGGTACTATGAGATTCAACTCAGGCACTCTCCGATTGCCAACCTGTCTC 2620
 QY 1589 CTGTGCAATGGGTTCACTGCTCCCTGATGCTGAGAGAGAGAGTGTGCAATTA 1648
 Db 2621 GTGTCTTGAGAGTTCAAGTTGTGTGTCTCCCAAGACAAAGAGAGTGTGCAACCA 2680
 QY 1649 CTGCCCCAGAGGTGTCAGTGTGCCGCTGAGAGCTGTGCTGATGGCTATTTTGGGA 1708
 Db 2681 CTGTCTTACTGCAACCACTGTGTAAGAGATGTGAGCTCTGTGATGATGGCTACTTGTGAGA 2740
 QY 1709 CCCCTTGGGGAACGTGCGCCAGTGAAGGCTGTGTCAAGCCCTGTCAGTGCACACAACGT 1768
 Db 2741 CCCCTGGGTAAAGAGCGCCTGTGAGACTTGGCCCTGTGCAAGTGCAGTGCACACAAT 2800
 QY 1769 GGACCTTATGCTCCGGAATGTGACCGCCTGACAGGCAAGTGTGTAAGTGCATCCA 1828
 Db 2801 CGATCCCAACGCAAGTTGAAATGCAATCGCTTGAGCGGAGAAATGCTGAAAGTGCATCTA 2860

QY 1829 CAACAGAGCTGGGGTCCACTGTGACCCAGTGCAGAAAGCAGGCTACTATGGGAGCCGTTGGC 1888
 Db 2861 TAACTGCTGGCTTCTATTTGTGACCGGAGGATTTTGGAAATCCCGCTGGC 2920
 QY 1889 TCCCAATCCAGCAGACAAAGTGTGAGCTTGCAACTGCAACCC 1930
 Db 2921 TCCCAATCCAGCAGACAAATGCAAAAGCTGTCAATTGCAATCC 2962

Search completed: July 6, 2003, 08:58:42
 Job time : 608 secs